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OM protein - protein search, using sw model

Run on: December 9, 2004, 08:39:26 ; Search time 5.05036 Seconds
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923.396 Million cell updates/sec

Title: US-09-462-416-1
Perfect score: 67
Sequence: 1 EFGAGLVLCGQPM 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues
Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23sep04:*
1: geneseqp19808:*
2: geneseqp19808:*
3: geneseqp20008:*
4: geneseqp20008:*
5: geneseqp20028:*
6: geneseqp20038:*
7: geneseqp20038:*
8: geneseqp20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Match Length	DB	ID	Description
1	67	100.0	13	AA03165	Aa03165 Linker us
2	67	100.0	13	AAU11643	Aau11643 Interleuk
3	67	100.0	13	ABG70576	Abg70576 Secretd
4	67	100.0	13	ABR44230	Ab44230 Linker pe
5	67	100.0	21	AA125368	Aay25368 IFNAR2/IF
6	67	100.0	34	AA125369	Aay25369 IFNAR2/IF
7	42	62.7	360	ABO70163	Ab070163 Pseudom
8	41	61.2	199	AAV37561	Aay37561 Protein i
9	41	61.2	291	ADM98607	Adm98607 Geranylge
10	41	61.2	623	ABR53138	Ab53138 Protein s
11	41	61.2	623	ADK63100	Adk63100 Disease t
12	41	61.2	640	ABO78796	Ab078796 Pseudom
13	41	61.2	920	AA866456	Aab66456 Protein e
14	41	61.2	920	ABR55195	Ab55195 Nucleotid
15	40	59.7	57	AAU51976	Aau51976 Propionib
16	40	59.7	57	ABM48495	Abm48495 Propionib
17	40	59.7	171	ABO83978	Ab083978 Pseudom
18	40	59.7	406	ABM65541	Abm65541 Propionib
19	40	59.7	805	ABB61739	Abb61739 Drosophi
20	40	59.7	875	ADU69760	Adu69760 Human hea
21	39	58.2	220	AA111027	Aay11027 H. pylori
22	39	58.2	220	AAW98208	Aaw98208 H. pylori
23	39	58.2	220	AA117195	Aay117195 H. pylori
24	39	58.2	419	ABU22234	Abu22234 Protein e
25	39	58.2	450	AD86082	Ad86082 Streptomy

26	39	58.2	770	6	ABR53218	Ab53218 Protein s
27	39	58.2	770	7	ADK63726	Adk63726 Disease t
28	39	58.2	810	6	ABJ26177	Abj26177 Apep911
29	39	58.2	811	6	ABJ25577	Abj25577 Apep911
30	38.5	57.5	903	7	ABO76231	Ab076231 Pseudom
31	38	56.7	191	3	AA035239	Aa035239 Zea mays
32	38	56.7	192	3	AA035238	Aa035238 Zea mays
33	38	56.7	202	3	AA040537	Aa040537 Arabidops
34	38	56.7	202	3	AA040531	Aa040531 Arabidops
35	38	56.7	249	3	AA040536	Aa040536 Arabidops
36	38	56.7	249	3	AA040530	Aa040530 Arabidops
37	38	56.7	249	3	AA035237	Aa035237 Zea mays
38	38	56.7	249	4	ABB62955	Abb62955 Drosophi
39	38	56.7	249	4	ABB65352	Abb65352 Drosophi
40	38	56.7	249	8	ADN73077	Adn73077 Thale cre
41	38	56.7	287	3	AA040535	Aa040535 Arabidops
42	38	56.7	289	3	AA040529	Aa040529 Arabidops
43	38	56.7	384	4	AA063834	Aa063834 Propionib
44	38	56.7	384	6	ABM60353	Abm60353 Propionib
45	38	56.7	388	3	AA013358	Aa013358 Arabidops

ALIGNMENTS

RESULT 1
AA03165
ID AA03165 standard; protein; 13 AA.
XX
AC AA03165;
XX
DT 11-JUN-1999 (first entry)
XX
DB Linker used in Chimeric sIL-6R/IL-6 protein.
XX
KW Soluble interleukin-6 receptor; interleukin-6; sIL-6; IL-6; sIL-6/IL-6;
KW Chimeric protein; fusion protein; cell growth inhibitor; melanoma cell;
KW highly malignant cancer cell; in vivo engraftment; mammalian cancer;
KW human hematopoietic cell; bone marrow transplantation; mammalian cancer;
KW hepatotoxic agent protection; haematopoiesis; liver disorder;
KW neurological disorder.
XX
OS Synthetic.
XX
PN WO902552-A2.
XX
PD 21-JAN-1999.
XX
PF 09-JUL-1998; 98WO-IL000321.
XX
PR 10-JUL-1997; 97IL-00121284.
PR 30-DEC-1997; 97IL-00122818.
XX
PA (YEDA) YEDA RES & DEV CO LTD.
XX
PI Revel M, Chebath J, Lapidot T, Kollet O;
XX
DR MPI, 1999-120776/10.
XX
PT New glycosylated soluble IL-6 receptor/IL-6 conjugates - used for e.g.
PT treating cancers, bone marrow transplantation, increasing haematopoiesis
PT or treating liver or neurological disorders.
XX
PS Claim 5; Page 54; 77pp; English.
XX
CC This sequence represents a linker that can be used in the chimeric
CC glycosylated soluble interleukin-6 receptor (sIL-6R)-interleukin-6 (IL-6)
CC protein (sIL-6R/IL-6) of the invention. The sIL-6R/IL-6 protein comprises
CC a fusion protein product between all of the naturally occurring form of
CC sIL-6R and all of the naturally occurring form of IL-6, the sIL-6/IL-6
CC and analogues being glycosylated in a similar fashion to the
CC glycosylation of naturally occurring sIL-6R and IL-6. The sIL-6R/IL-6 and
CC analogues are capable of inhibiting the growth of highly malignant cancer

CC cells, e.g. melanoma cells, eliciting the in vivo engraftment of human
 CC haematopoietic cells in bone marrow transplantation and protecting liver
 CC from hepatotoxic agents. They can be used for the preparation of a
 CC medicament for treating mammalian cancers by way of inhibition of cancer
 CC cells, for enhancement of bone marrow transplantation by way of eliciting
 CC engraftment of human haematopoietic cells in bone marrow transplantation,
 CC for increasing haematopoiesis, for treating liver or neurological
 CC disorders, or in other applications in which IL-6 or sIL-6R are used
 XX

Sequence 13 AA;

Query Match 100.0%; Score 67; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.00045;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EFGAGLVGGQFM 13
 1 EFGAGLVGGQFM 13

RESULT 2

ID AAU1643 standard; protein; 13 AA.

AC AAU1643;

DT 12-MAR-2002 (first entry)

DE Interleukin 18 (IL-18)/immunoglobulin, linker peptide.

KM Interleukin 18; IL-18; cytokine; interleukin-18 inhibitor;
 KM atherosclerosis; cardiant; vasotropic; antilicer; myocardial infarction;
 KM atherosclerotic plaque; thrombosis of atherosclerotic plaque; stroke;
 KM ischemic syndrome; heart failure; arteriosclerosis; vascularisation;
 KM atheroma; immunoglobulin, linker peptide.
 XX

OS Synthetic.

PN WO200185201-A2.

PD 15-NOV-2001.

PF 30-APR-2001; 2001WO-EP004843.

PR 05-MAY-2000; 2000EP-00109606.

PA (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV,
 (INRM) INSERM INST NAT SANTE & RECH MEDICALE.

PI Chvatchko Y, Tedgui A, Mallat Z,

DR WPI; 2002-075227/10.

PT Use of interleukin-18 inhibitor for manufacture of medicament for
 PT treatment and/or prevention of atherosclerosis, thrombosis of
 PT atherosclerotic plaque, atherosclerotic plaque ulcer and heart failure
 PT recurrent events.
 XX

PS Disclosure; Page 16; 54pp; English.

CC The invention describes the use of interleukin-18 (IL-18) inhibitor for
 CC manufacture of medicament for treatment and/or prevention of diseases or
 CC as diagnostic marker for had clinical prognosis in heart failure or
 CC recurrent events after first event of heart failure or
 CC is useful for: the manufacture of a medicament for treatment and/or
 CC prevention of atherosclerosis/arteriosclerosis; the manufacture of a
 CC medicament for treatment and/or prevention of thrombosis of
 CC atherosclerotic plaque (AP), AP ulcer, AP destabilisation (responsible
 CC for stroke), atheroma, ischemic syndromes e.g. myocardial infarction, AP
 CC disruption or heart failure recurrent events e.g. death, recurrent
 CC ischemia, re-vascularisation and progression of atherosclerosis, where
 CC the heart failure is ischaemic or non-ischaemic and as a diagnostic

CC marker for bad clinical prognosis in heart failure or recurrent events
 CC after first event of heart failure. This sequence is an example of a
 CC peptide linker used to create fusion proteins of Interleukin-18 (IL-18)
 CC with all or part of an immunoglobulin, discussed in the invention
 XX

Sequence 13 AA;

Query Match 100.0%; Score 67; DB 5; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.00045;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EFGAGLVGGQFM 13
 1 EFGAGLVGGQFM 13

RESULT 3

ID ABG70576 standard; peptide; 13 AA.

AC ABG70576;

DT 29-NOV-2002 (first entry)

DE Secreted apoptosis-related protein 1 (SARP-1) linker peptide.

KM Secreted apoptosis-related protein 1; SARP-1; scleroderma;
 KM systemic sclerosis; fibrotic disease; liver cirrhosis; Keloid;
 KM interstitial pulmonary fibrosis; Dupuytren's contracture; scarring;
 KM wound healing; postoperative adhesion; reactive fibrosis;
 KM chronic heart failure; myocardial infarction; inflammatory disorder;
 KM lung inflammation; idiopathic pulmonary fibrosis; systemic disease;
 KM rheumatoid arthritis; anti-sclerotic; immunoglobulin.
 XX

OS Synthetic.

PN WO200246225-A2.

PD 13-JUN-2002.

PF 30-NOV-2001; 2001WO-EP013992.

PR 06-DEC-2000; 2000EP-00126771.

PR 17-AUG-2001; 2001EP-00118888.

PA (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.

PI Plater-Zyberk C, Power C, Collinge J;

DR WPI; 2002-706807/76.

PT Use of human Secreted Apoptosis-Related Protein (SARP)-1 and SARP-1
 PT nucleic acids for the treatment of sclerosis, especially systemic
 PT sclerosis.
 XX

PS Disclosure; Page 15; 63pp; English.

CC The present invention relates to the use of human secreted apoptosis-
 CC related protein 1 (SARP-1), SARP-1 nucleic acids and/or a substance which
 CC stimulates the release or potentiates the activity of endogenous SARP-1
 CC for the treatment of scleroderma. The SARP-1 protein binds to and
 CC initiates signalling of the human SARP-1 receptor. The SARP-1 protein can
 CC be used in protein therapy, and the polynucleotide sequences encoding
 CC SARP-1 can be used in gene therapy. SARP-1 polypeptide and polynucleotide
 CC sequences, and pharmaceutical compositions comprising SARP-1 are useful
 CC for the treatment of scleroderma; especially systemic sclerosis. They may
 CC also be used to treat fibrotic diseases (e.g. liver cirrhosis,
 CC interstitial pulmonary fibrosis, Dupuytren's contracture, keloid and
 CC other scarring/wound healing abnormalities), postoperative adhesions and
 CC reactive fibrosis), chronic heart failure (particularly after myocardial
 CC infarction), disorders involving inflammation of the lung (e.g.
 CC idiopathic pulmonary fibrosis), and systemic diseases (e.g. rheumatoid
 CC arthritis). The present sequence represents a linker peptide that can be

CC used to fuse SARP-1 to an immunoglobulin to form a fusion protein
XX
SQ Sequence 13 AA;

Query Match 100.0%; Score 67; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00045;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EFGAGLVIGGQFM 13
DB 1 EFGAGLVIGGQFM 13

RESULT 4
ABR44230
ID ABR44230 standard; peptide; 13 AA.

AC ABR44230;

DT 18-AUG-2003 (first entry)

DE Linker peptide used in constructing an IL-6R/IL-6 chimera.

XX IL-6; gp130; interleukin-6; antidiabetic; neuroprotective; gene therapy;
KW linker.

OS Synthetic.

PN WO2003033015-A1.

PD 24-APR-2003.

PF 10-OCT-2002; 2002WO-EP011364.

PR 11-OCT-2001; 2001EP-00123400.

PA (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.

PI Dreano M, Vitte P;

DR WPI/ 2003-403150/38.

XX Use of a substance signaling through gp130, or use of a vector for
XX inducing and/or enhancing endogenous production of interleukin-6 in cell,
PT for preparing a medicament for treating and preventing diabetic
PT neuropathy.

PS Disclosure; Page 17; 85pp; English.

XX The invention relates to the use of a substance (I) signaling through
CC gp130, or use of a vector (II) for inducing and/or enhancing the
CC endogenous production of interleukin-6 (IL-6) in a cell. (I), (II) or a
CC cell expressing (I), is useful in the manufacture of a medicament for the
CC treatment and/or prevention of diabetic neuropathy. (I) is useful for
CC treating or preventing diabetic neuropathy such as polyneuropathy or
CC mononeuropathy. The present sequence represents a linker peptide used for
CC constructing an IL-6R/IL-6 chimera

XX Sequence 13 AA;

Query Match 100.0%; Score 67; DB 6; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00045;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EFGAGLVIGGQFM 13
DB 1 EFGAGLVIGGQFM 13

RESULT 5
AAV25368
ID AAV25368 standard; peptide; 21 AA.
XX

AC AAV25368;
XX
DT 06-SEP-1999 (first entry)

DE IFNAR2/IFN-beta complex peptide fragment 11.

XX IFNAR2; IFN-beta; type I interferon; IFNAR/IFN complex; IFN; antiviral;
KW human interferon alpha/beta receptor; anticancer; immunomodulatory;
KW anti-arthritis; antidiabetic; treatment; hepatitis; viral infection;
KW hairy cell leukemia; Kaposi's sarcoma; multiple myeloma; cancer; lupus;
KW diabetes; multiple sclerosis; rheumatoid arthritis; myasthenia gravis;
KW acquired immune deficiency syndrome.

OS Synthetic.

PN WO9932141-A1.

PD 01-JUL-1999.

PF 18-DEC-1998; 96WO-US026926.

PR 19-DEC-1997; 97US-0068295P.

PA (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.
(MCIN/) MCINNIS P G.

PI Tepper M, Cunningham M, Sherrie D, El Tayer N, McKenna S;

DR WPI/ 1999-405115/34.

XX Prolonging in vivo activity of type I interferon by complexing.

PS Disclosure; Page 80; 86pp; English.

XX This invention describes a novel method for prolonging the in vivo effect
CC of type I interferon (IFN) by administering IFN as a complex (A) with a
CC subunit (I) of the human interferon alpha/beta receptor (IFNAR). The
CC product of the invention has antiviral, anticancer, immunomodulatory,
CC anti-arthritis and antidiabetic activity. (A) have the antiviral,
CC anticancer and immunomodulating activities of IFN, e.g. for treating
CC hepatitis and other viral infections, hairy cell leukemia, Kaposi's
CC sarcoma, multiple myeloma and other cancers, multiple sclerosis,
CC rheumatoid arthritis, myasthenia gravis, diabetes, acquired immune
CC deficiency syndrome and lupus. When complexed in (A), the storage life of
CC IFN is increased (i.e. it is stabilized against oligomerization, without
CC the need for storage at acidic pH) and its biological effect is
CC potentiated

XX Sequence 21 AA;

Query Match 100.0%; Score 67; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.00074;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EFGAGLVIGGQFM 13
DB 6 EFGAGLVIGGQFM 18

RESULT 6
AAV25369

ID AAV25369 standard; peptide; 34 AA.

XX AAV25369;

DT 06-SEP-1999 (first entry)

DE IFNAR2/IFN-beta complex peptide fragment 12.

XX IFNAR2; IFN-beta; type I interferon; IFNAR/IFN complex; IFN; antiviral;
KW human interferon alpha/beta receptor; anticancer; immunomodulatory;
KW anti-arthritis; antidiabetic; treatment; hepatitis; viral infection;
KW hairy cell leukemia; Kaposi's sarcoma; multiple myeloma; cancer; lupus;

KM diabetes; multiple sclerosis; rheumatoid arthritis; myasthenia gravis;
 KM acquired immune deficiency syndrome.
 XX Synthetic.
 OS
 XX WO9932141-A1.
 XX
 PD 01-JUL-1999.
 XX
 PF 18-DEC-1998; 98WO-US026926.
 XX
 PR 19-DEC-1997; 97US-0068295P.
 XX
 PA (ISTF) ARS APPLIED RRS SYSTEMS HOLDING NV.
 MCIN/ MCINNIS P G.
 XX
 PI Tepper W, Cunningham M, Sherris D, El Tayar N, McKenna S;
 DR WPI; 1999-405115/34.
 XX
 PT Prolonging in vivo activity of type I interferon by complexing.
 PS Disclosure; Page 80; 86pp; English.
 XX
 CC This invention describes a novel method for prolonging the in vivo effect
 of type I interferon (IFN) by administering IFN as a complex (A) with a
 CC subunit (I) of the human interferon alpha/beta receptor (IFNAR). The
 CC product of the invention has antiviral, anticancer, immunomodulatory,
 CC anti-arthritic and antidiabetic activity. (A) have the antiviral,
 CC anticancer and immunomodulating activities of IFN, e.g. for treating
 CC hepatitis and other viral infections, hairy cell leukemia, Kaposi's
 CC sarcoma, multiple myeloma and other cancers, multiple sclerosis,
 CC rheumatoid arthritis, myasthenia gravis, diabetes, acquired immune
 CC deficiency syndrome and lupus. When complexed in (A), the storage life of
 CC IFN is increased (i.e. it is stabilized against oligomerization, without
 CC the need for storage at acidic pH) and its biological effect is
 CC potentiated
 XX
 SQ Sequence 34 AA;
 Query Match 100.0%; Score 67; DB 2; Length 34;
 Best Local Similarity 100.0%; Pred. No. 0.0012;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EFGAGLVGGQFM 13
 DB 6 EFGAGLVGGQFM 18
 RESULT 7
 ABO70163
 ID ABO70163 standard; protein; 360 AA.
 XX
 AC ABO70163;
 XX
 DT 29-JUL-2004 (first entry)
 XX
 DE Pseudomonas aeruginosa polypeptide #2338.
 XX
 KM Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
 XX
 OS Pseudomonas aeruginosa.
 XX
 PN US6551795-B1.
 XX
 PD 22-APR-2003.
 XX
 PF 18-FEB-1999; 99US-00252991.
 XX
 PR 18-FEB-1998; 98US-0074788P.
 PR 27-JUL-1998; 98US-0094190P.
 XX
 PA (GENO-) GENOME THERAPEUTICS CORP.

XX
 PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;
 XX WPI; 2003-615309/58.
 DR N-PsDB; ABD03734.
 XX
 PT Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
 PT useful as molecular targets for diagnostics, prophylaxis and treatment of
 PT pathological conditions resulting from bacterial infection.
 XX
 PS Disclosure; SEQ ID NO 18909; 455pp; English.
 XX
 CC The invention relates to Pseudomonas aeruginosa polypeptides and the
 CC polynucleotides encoding them. The sequences are useful in diagnosis and
 CC therapy of pathological conditions, as molecular targets for diagnostics,
 CC prophylaxis and treatment of pathological conditions resulting from a
 CC bacterial infection, for evaluating a compound, such as a polypeptide,
 CC for the ability to bind a P. aeruginosa nucleic acid, as components of
 CC effective antibacterial targets, as targets for antibacterial drugs,
 CC including anti-P. aeruginosa drugs, as templates for recombinant
 CC production of P. aeruginosa-derived peptides or polypeptides, as target
 CC components for diagnosis and/or treatment of P. aeruginosa-caused
 CC infection, and in detection of P. aeruginosa sequences or other sequences
 CC of Pseudomonas species using biochip technology. Sequences ABO67826-
 CC ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification but was obtained in electronic format from USPTO at
 CC seqdata.uspto.gov/sequence.html
 XX
 SQ Sequence 360 AA;
 Query Match 62.7%; Score 42; DB 7; Length 360;
 Best Local Similarity 80.0%; Pred. No. 1.5e+02;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 3 GAGLVGGQF 12
 DB 202 GAALLGGQF 211
 RESULT 8
 AAY37561
 ID AAY37561 standard; protein; 199 AA.
 XX
 AC AAY37561;
 XX
 DT 07-OCT-1999 (first entry)
 XX
 DE Protein involved in intermediate metabolism of fatty acids.
 XX
 KM Vaccine; eye disease; conventional trachoma; nonendemic trachoma;
 KM paratrachoma; inclusion conjunctivitis; genital disease; perilepitis;
 KM nongonococcal urethritis; epididymitis; cervicitis; salpingitis;
 KM Bartholinitis; pneumopathy; venereal lymphogranulomatosis.
 XX
 OS Chlamydia trachomatis.
 XX
 PN WO9928475-A2.
 XX
 PD 10-JUN-1999.
 XX
 PF 27-NOV-1998; 98WO-IB001939.
 XX
 PR 28-NOV-1997; 97FR-00015041.
 PR 17-DEC-1997; 97FR-00015034.
 PR 04-NOV-1998; 98US-0107077P.
 XX
 PA (GEST) GENSET.
 XX
 PI Grifffais R;
 XX
 DR WPI; 1999-371125/31.
 XX

PT Genome sequence of Chlamydia trachomatis.
 XX Disclosure; Page 1221; 1755pp; English.
 XX
 XX
 CC AAY36754-y37949 are encoded by open reading frames (ORFs) of the genome
 CC of Chlamydia trachomatis (see AA201425). The polypeptides can be used as
 CC vaccines against Chlamydia trachomatis. Antisense and ribozyme sequences
 CC can also be used to control growth of the microorganism. Chlamydia
 CC trachomatis is responsible for a large number of diseases, e.g. eye
 CC diseases such as conventional trachoma, nongonococcal urethritis,
 CC paratrachoma, and inclusion conjunctivitis; genital diseases such as
 CC nongonococcal urethritis, epididymitis, cervicitis, salpingitis,
 CC perhepatitis, bartonellosis, pneumopathy in breast feeding infants; and
 CC venereal lymphogranulomatosis. The polypeptides of the invention may be
 CC of use in treating these diseases
 XX
 SQ Sequence 199 AA;
 Query Match 61.2%; Score 41; DB 2; Length 199;
 Best Local Similarity 63.6%; Pred. No. 1.2e+02;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 2 FGAGLVGGQF 12
 DB 61 FGVGILGGQY 71
 RESULT 9
 ADM98607
 ID ADM98607 standard; protein; 291 AA.
 XX
 AC ADM98607;
 XX
 DT 01-JUL-2004 (first entry)
 XX
 DE Geranylgeranyl pyrophosphate synthase polypeptide #6.
 XX
 KM Geranylgeranyl pyrophosphate synthase; diterpene precursor;
 KM diterpene synthase; defence toxin; volatile defensive signal;
 KM pollinator attractant; photoprotectant; enzyme.
 XX
 OS Chlamydia trachomatis.
 OS
 XX US2004072323-A1.
 PN
 XX 15-APR-2004.
 PD
 XX 07-JAN-2002; 2002US-00041018.
 PF
 XX 05-JAN-2001; 2001US-0259880P.
 PR
 XX (MATS/) MATSUDA S P T.
 PA (HART/) HART E A.
 XX
 PI Matsuda SPT, Hart EA;
 PI
 DR WPI; 2004-373921/35.
 XX
 PT New unicellular organisms comprising exogenous nucleic acids encoding a
 PT geranylgeranyl pyrophosphate and a diterpene synthase, useful for
 PT producing diterpenes and diterpene precursors.
 PT
 XX Claim 30; SEQ ID NO 27; 38pp; English.
 PS
 XX The invention relates to a unicellular organism for producing a diterpene
 CC or diterpene precursor comprising an exogenous nucleic acid sequence
 CC encoding a geranylgeranyl pyrophosphate synthase under the control of a
 CC promoter operable in the organism, and an exogenous nucleic acid sequence
 CC encoding a diterpene synthase under the control of a promoter operable in
 CC the organism. The invention also relates to methods of producing a
 CC diterpene or diterpene precursor and a method of isolating a diterpene
 CC synthase comprising growing several cells in the presence of a
 CC polyaromatic resin to make a cell/resin mixture, where at least one of

CC the cells further comprises at least one isolated and purified nucleic
 CC acid sequence of a yeast expression library, and the expression of the
 CC nucleic acid sequence is regulated by an inducible promoter under
 CC conditions where the expression is induced, filtering the cell/resin
 CC mixture, extracting the cell/resin mixture with alcohol to produce an
 CC organic eluent and analysing the organic eluent by a screening method
 CC including chromatography and/or spectroscopy, to identify the nucleic
 CC acid sequence encoding the diterpene synthase. The unicellular
 CC microorganism is useful as a diterpene or diterpene precursor producing
 CC system. Diterpenes, in plants, serve as defence toxins, volatile
 CC defensive signals, pollinator attractants and photoprotectants. This
 CC sequence represents a geranylgeranyl pyrophosphate synthase polypeptide
 CC of the invention. Note: The sequence data for this patent did not form
 CC part of the printed specification but was obtained in electronic format
 CC from USPTO at seqdata.uspto.gov/sequence.html.
 XX
 SQ Sequence 291 AA;
 Query Match 61.2%; Score 41; DB 8; Length 291;
 Best Local Similarity 63.6%; Pred. No. 1.8e+02;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 2 FGAGLVGGQF 12
 DB 153 FGVGILGGQY 163
 RESULT 10
 ABR53138
 ID ABR53138 standard; protein; 623 AA.
 XX
 AC ABR53138;
 XX
 DT 20-JUN-2003 (first entry)
 XX
 DE Protein sequence #SEQ ID 1141.
 XX
 DE Multiprotein complex; eukaryote; drug target; diagnosis.
 XX
 KM Saccharomyces cerevisiae.
 KM
 OS
 XX EP1258494-A1.
 PN
 XX 20-NOV-2002.
 PD
 XX 20-DEC-2001; 2001EP-00130253.
 PF
 XX 15-MAY-2001; 2001EP-00111774.
 PR
 XX (CELL-) CELLZONE AG.
 PA
 XX Bauer A, Gavin A, Grandi P, Krause R, Kruse UD, Kuester BD;
 PI Marzloch M, Schultz JD, Superti-Furga GD;
 PI
 DR WPI; 2003-250078/25.
 XX
 DR N-PSDB; ACC61180.
 XX
 PT New isolated protein complexes useful for diagnosing a disease or
 PT disorder, or as a target for an active agent of a pharmaceutical,
 PT preferably a drug target in the treatment or prevention of disease or
 PT disorder.
 PT
 XX Disclosure; SEQ ID NO 1141; 17pp + Sequence Listing; English.
 PS
 XX The invention relates to multiprotein complexes from eukaryotes. Proteins
 CC of the invention and DNA sequences encoding them are given in records
 CC ABR52568-ABR53903 and ACC60610-ACC61944 respectively. The complexes are
 CC obtainable by using a protein as a bait and isolating the set of proteins
 CC which is attached thereto from cells. Such protein complexes may comprise
 CC up to 30 distinct proteins. Protein complexes of the invention are useful
 CC for diagnosing a disease or disorder, or as a target for an active agent
 CC of a pharmaceutical, preferably a drug target in the treatment or
 CC prevention of a disease or disorder. Note: The sequence data for this

CC patent is not represented in the printed specification, but is based on
CC sequence information supplied by the European Patent Office. The complete
CC document is available on CD-ROM
XX
SQ Sequence 623 AA;

Query Match 61.2%; Score 41; DB 6; Length 623;
Best Local Similarity 63.6%; Pred. No. 4e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 EFGAGLVGGQ 11
Db 194 EFGASVYAGGQ 204

RESULT 11
ADK63100
ID ADK63100 standard; protein; 623 AA.

XX ADK63100;

XX 06-MAY-2004 (first entry)

XX Disease treating protein complex-derived protein #676.

XX protein complex; drug target; diagnosis.

XX Unidentified.

XX EPI338608-A2.

XX 27-AUG-2003.

XX 20-DEC-2002; 2002EP-00102902.

XX 20-DEC-2001; 2001EP-00130253.

XX (CELL-) CELLZONE AG.

XX Bauer A, Gavin A, Superti-Furga G, Kuester B, Schultz J;

XX Merzloch M, Grandi P, Krause R, Krause U, Merino A, Bauch A;

XX Michon A, Leutwein C, Rick J;

XX WPI; 2003-638460/61.

XX N-PSDB; ADK63101.

XX New proteins and protein complexes from eukaryotes, useful as targets in
PT drug screening, or in diagnosing or screening for the presence of a
PT disease or disorder, or a predisposition for developing a disease or
PT disorder in a subject.

XX Disclosure; SEQ ID NO 1351; 13pp; English.

XX The invention relates to novel protein complexes comprising a first and a
CC second protein, or its derivative, fragment, homologue or variant. The
CC proteins are selected from given protein complexes, which are not defined
CC in the specification. The variants are encoded by nucleic acids that
CC hybridize to the nucleic acids encoding the proteins under low stringency
CC conditions. The protein complexes are useful as targets for an active
CC agent of a pharmaceutical. These protein complexes are particularly
CC useful as drug targets for the treatment or preventing of a disease or
CC disorder. The complexes and methods above are useful in diagnosing or
CC screening for the presence of a disease or disorder or a predisposition
CC for developing a disease or disorder in a subject. These are also useful
CC in screening for a drug for treatment or prevention of a disease or
CC disorder. The molecule that modulates the amount, activity or protein
CC components of the complex is useful for the manufacture of a medicament
CC for the treatment or prevention of a disease or disorder. This sequence
CC corresponds to a protein of the invention. (Note: the sequence data for
CC this patent did not form part of the printed specification but was
CC obtained from the EPO in electronic format.)

XX Sequence 623 AA;

Query Match 61.2%; Score 41; DB 7; Length 623;
Best Local Similarity 63.6%; Pred. No. 4e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 EFGAGLVGGQ 11
Db 194 EFGASVYAGGQ 204

RESULT 12
ABO78796
ID ABO78796 standard; protein; 640 AA.

XX ABO78796;

XX 29-JUL-2004 (first entry)

XX Pseudomonas aeruginosa polypeptide #10971.

XX Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.

XX Pseudomonas aeruginosa.

XX US6551795-B1.

XX 22-APR-2003.

XX 18-FEB-1999; 99US-00252991.

XX 18-FEB-1998; 98US-0074788P.

XX 27-JUL-1998; 98US-0094190P.

XX (GENO-) GENOME THERAPEUTICS CORP.

XX Rubenfield MJ, Nolling J, Deloughery C, Bush D;

XX WPI; 2003-615309/58.

XX N-PSDB; ABD12367.

XX Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
PT useful as molecular targets for diagnostics, prophylaxis and treatment of
PT pathological conditions resulting from bacterial infection.

XX Disclosure; SEQ ID NO 27542; 455pp; English.

XX The invention relates to Pseudomonas aeruginosa polypeptides and the
CC polynucleotides encoding them. The sequences are useful in diagnosis and
CC therapy of pathological conditions, as molecular targets for diagnostics,
CC prophylaxis and treatment of pathological conditions resulting from a
CC bacterial infection, for evaluating a compound, such as a polypeptide,
CC for the ability to bind a P. aeruginosa nucleic acid, as components of
CC effective antibacterial targets, as targets for antibacterial drugs,
CC including anti-P. aeruginosa drugs, as templates for recombinant
CC production of P. aeruginosa-derived peptides or polypeptides, as target
CC components for diagnosis and/or treatment of P. aeruginosa-caused
CC infection, and in detection of P. aeruginosa sequences or other sequences
CC of Pseudomonas species using biochip technology. Sequences ABO67826-
CC ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html

XX Sequence 640 AA;

Query Match 61.2%; Score 41; DB 7; Length 640;
Best Local Similarity 80.0%; Pred. No. 4.1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 EFGAGLVGGQ 11
Db 304 FPAAGLVGGQ 313


```

XX PN WO200181581-A2.
XX
XX 01-NOV-2001.
XX
XX 20-APR-2001; 2001WO-US012865.
XX
XX 21-APR-2000; 2000US-0199047P.
XX 02-JUN-2000; 2000US-0208841P.
XX 07-JUL-2000; 2000US-0216747P.
XX
XX (CORI-) CORIXA CORP.
XX
XX Skeiky YAM, Persing DH, Mitcham JL, Wang SS, Bhatia A,
XX L' Maisonneuve J, Zhang Y, Jen S, Carter D;
XX WPI; 2001-616774/71.
XX N-PSDB; AAS59553.
XX
XX Propionibacterium acnes polypeptides and nucleic acids useful for
XX vaccinating against and diagnosing infections, especially useful for
XX treating acne vulgaris.
XX
XX Example 1; SEQ ID NO 13171, 1069pp; English.
XX
XX Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
XX polypeptides. The proteins and their associated DNA sequences are used in
XX the treatment, prevention and diagnosis of medical conditions caused by
XX P. acnes. The disorders include SAPRO syndrome (synovitis, acne,
XX pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
XX P. acnes is also involved in infections of bone, joints and the central
XX nervous system, however it is particularly involved in the inflammatory
XX lesions associated with acne vulgaris. A method for detecting the
XX presence or absence of P. acnes in a patient comprises contacting a
XX sample with a binding agent that binds to the proteins of the invention
XX and determining the amount of bound protein in the sample. The
XX polypeptides may be used as antigens in the production of antibodies
XX specific for P. acnes proteins. These antibodies can be used to
XX downregulate expression and activity of P. acnes polypeptides and
XX therefore treat P. acnes infections. The antibodies may also be used as
XX diagnostic agents for determining P. acnes presence, for example, by
XX enzyme linked immunosorbent assay (ELISA). Note: The sequence data for
XX this patent did not form part of the printed specification, but was
XX obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 57 AA;
XX
XX Query Match 59.7%; Score 40; DB 4; Length 57;
XX Best Local Similarity 80.0%; Pred. No. 47;
XX Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 2 FGAGLVLAGGQ 11
XX DB 43 FGAGLVYAGQ 52
XX
XX RESULT 16
XX ID ABM48495 standard; protein; 57 AA.
XX
XX ABM48495;
XX
XX 20-OCT-2003 (first entry)
XX
XX Propionibacterium acnes predicted ORF-encoded polypeptide #13171.
XX
XX Acne vulgaris; antiseborrheic; dermatological; antibacterial;
XX immunostimulant; immune response; vaccine.
XX
XX Propionibacterium acnes.
XX
XX WO2003033515-A1.
XX PN

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XX 24-APR-2003.
XX
XX 11-OCT-2002; 2002WO-US032727.
XX
XX 15-OCT-2001; 2001US-00978825.
XX
XX (CORI-) CORIXA CORP.
XX
XX Mitcham JL, Skeiky YAM, Persing DH, Bhatia A, Maisonneuve JL;
XX Zhang Y, Wang S, Jen S, Lodes WD, Benson DR, Jones R, Carter D;
XX Barth B, Valiieve-Douglas J;
XX WPI; 2003-381769/36.
XX N-PSDB; ACF64482.
XX
XX New Propionibacterium acnes polypeptides and polynucleotides encoding the
XX polypeptide, useful for diagnosing, preventing or treating acne vulgaris,
XX or for stimulating an immune response specific for a P. acnes protein.
XX
XX Example 1; SEQ ID NO 13171, 1481pp; English.
XX
XX The invention relates to an isolated polynucleotide (ACF64435-ACF64733)
XX encoding a Propionibacterium acnes protein. The invention also relates to
XX polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to
XX immunogenic fragments of P. acnes polypeptides. The invention
XX additionally encompasses expression vectors and host cells comprising a
XX polynucleotide of the invention; antibodies against polypeptides of the
XX invention; fusion proteins comprising a polypeptide of the invention; a
XX method for stimulating an immune response specific for a P. acnes
XX polypeptide and an isolated T cell population comprising T cells prepared
XX via this method; a vaccine composition (comprising P. acnes polypeptides,
XX polynucleotides, antibodies, fusion proteins, T cell populations, or
XX antigen-presenting cells that express the polypeptide); a method and kit
XX for detecting or determining the presence or absence of P. acnes in a
XX patient; and a method for inhibiting the development of P. acnes in a
XX patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion
XX proteins, T cell populations or antigen-presenting cells that express the
XX polypeptides are useful for diagnosing, preventing or treating acne
XX vulgaris, or for stimulating an immune response specific for a P. acnes
XX protein. The polynucleotides can also be used as probes or primers for
XX nucleic acid hybridization. The vaccine composition is useful for the
XX stimulation of an immune response against P. acnes, or for treating acne,
XX and the kit is useful for performing a diagnostic assay. The present
XX sequence represents a polypeptide predicted to be encoded by an ORF (open
XX reading frame) contained within the P. acnes polynucleotides of the
XX invention. Note: The sequence data for this patent did not form part of
XX the printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 57 AA;
XX
XX Query Match 59.7%; Score 40; DB 6; Length 57;
XX Best Local Similarity 80.0%; Pred. No. 47;
XX Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 2 FGAGLVLAGGQ 11
XX DB 43 FGAGLVYAGQ 52
XX
XX RESULT 17
XX ID AB083978 standard; protein; 171 AA.
XX
XX AB083978;
XX
XX 29-JUL-2004 (first entry)
XX
XX Pseudomonas aeruginosa polypeptide #16153.
XX
XX Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
XX
XX PN

```

OS Pseudomonas aeruginosa.
 XX
 XX US6551795-B1.
 XX
 PD 22-APR-2003.
 XX
 PF 18-FEB-1999; 99US-00252991.
 XX
 PR 18-FEB-1998; 98US-0074788P.
 XX 27-JUL-1998; 98US-0094190P.
 XX
 PA (GENO-) GENOME THERAPEUTICS CORP.
 PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;
 XX
 PI MPI: 2003-615309/58.
 DR N-PSDB; ABD17549.
 DR
 XX
 PT Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
 PT useful as molecular targets for diagnostics, prophylaxis and treatment of
 PT pathological conditions resulting from bacterial infection.
 XX
 PS Disclosure; SEQ ID NO 32724; 455pp; English.
 XX
 CC The invention relates to Pseudomonas aeruginosa polypeptides and the
 CC polynucleotides encoding them. The sequences are useful in diagnosis and
 CC therapy of pathological conditions, as molecular targets for diagnostics,
 CC prophylaxis and treatment of pathological conditions resulting from a
 CC bacterial infection, for evaluating a compound, such as a polypeptide,
 CC for the ability to bind a P. aeruginosa nucleic acid, as components of
 CC effective antibacterial targets, as targets for antibacterial drugs,
 CC including anti-P. aeruginosa drugs, as templates for recombinant
 CC production of P. aeruginosa-derived peptides or polypeptides, as target
 CC components for diagnosis and/or treatment of P. aeruginosa-caused
 CC infection, and in detection of P. aeruginosa sequences or other sequences
 CC of Pseudomonas species using biocchip technology. Sequences AB067826-
 CC AB084396 represent P. aeruginosa polypeptides of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification but was obtained in electronic format from USPTO at
 CC seqdata.uspto.gov/Sequence.html
 CC
 XX
 SQ Sequence 171 AA;
 XX

Query Match 59.7%; Score 40; DB 7; Length 171;
 Best Local Similarity 77.8%; Pred. No. 1.5e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 7; Conservative 2;

QY 2 FGAGLVLG 10
 ||:|||||
 DB 101 FGSGLLGG 109

RESULT 18
 ABM65541
 ID ABM65541 standard; protein; 406 AA.
 XX
 AC ABM65541;
 XX
 DT 20-OCT-2003 (first entry)
 XX
 DE Propionibacterium acnes immunogenic polypeptide #30217.
 XX
 XX Acne vulgaris; antiseborrheic; dermatological; antibacterial;
 KM immunostimulant; immune response; vaccine; immunogenic.
 XX
 OS Propionibacterium acnes.
 XX
 XX WO2003033515-A1.
 PN
 XX 24-APR-2003.
 PD
 XX 11-OCT-2002; 2002WO-US032727.
 PF
 XX

PR 15-OCT-2001; 2001US-00978825.
 XX
 XX (CORI-) CORIXA CORP.
 XX
 PA Mitcham JL, Skelky YAW, Persing DH, Bhatia A, Maisonneuve JL;
 XX Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR, Jones R, Carter D;
 PI Barth B, Vailleve-Douglas J;
 XX
 DR MPI: 2003-381789/36.
 XX
 XX
 PT New Propionibacterium acnes polypeptides and polynucleotides encoding the
 PT polypeptide, useful for diagnosing, preventing or treating acne vulgaris,
 PT or for stimulating an immune response specific for a P. acnes protein.
 XX
 PS Claim 7; SEQ ID NO 30217; 1481pp; English.
 XX
 CC The invention relates to an isolated polynucleotide (ACF64435-ACF64733)
 CC encoding a Propionibacterium acnes protein. The invention also relates to
 CC polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to
 CC immunogenic fragments of P. acnes polypeptides. The invention
 CC additionally encompasses expression vectors and host cells comprising a
 CC polynucleotide of the invention; antibodies against polypeptides of the
 CC invention; fusion proteins comprising a polypeptide of the invention; a
 CC method for stimulating an immune response specific for a P. acnes
 CC polypeptide and an isolated T cell population comprising P. acnes polypeptides,
 CC via this method; a vaccine composition (comprising P. acnes polypeptides,
 CC polynucleotides, antibodies, fusion proteins, T cell populations, or
 CC antigen-presenting cells that express the polypeptide); a method and kit
 CC for detecting or determining the presence or absence of P. acnes in a
 CC patient; and a method for inhibiting the development of P. acnes in a
 CC patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion
 CC proteins, T cell populations or antigen-presenting cells that express the
 CC polypeptides are useful for diagnosing, preventing or treating acne
 CC vulgaris, or for stimulating an immune response specific for a P. acnes
 CC protein. The polynucleotides can also be used as probes or primers for
 CC nucleic acid hybridization. The vaccine composition is useful for the
 CC stimulation of an immune response against P. acnes, or for treating acne,
 CC and the kit is useful for performing a diagnostic assay. The present
 CC sequence represents a specifically claimed P. acnes polypeptide which is
 CC thought to contain an immunogenic region. Note: The sequence data for
 CC this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 CC
 XX
 SQ Sequence 406 AA;
 XX

Query Match 59.7%; Score 40; DB 6; Length 406;
 Best Local Similarity 80.0%; Pred. No. 3.7e+02; Mismatches 2; Indels 0; Gaps 0;
 Matches 8; Conservative 0;

QY 2 FGAGLVLG 11
 |||||
 DB 392 FGAGLVYAGQ 401

RESULT 19
 ABB61739
 ID ABB61739 standard; protein; 805 AA.
 XX
 AC ABB61739;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Drosophila melanogaster polypeptide SEQ ID NO 12009.
 XX
 XX Drosophila; developmental biology; cell signalling; insecticide;
 KM pharmaceutical.
 XX
 OS Drosophila melanogaster.
 XX
 XX WO200171042-A2.
 PN
 XX 27-SEP-2001.
 PD
 XX

XX 23-MAR-2001; 2001MO-US009231.
 PF 23-MAR-2000; 2000US-0191637P.
 XX 11-JUL-2000; 2000US-00614150.
 PR (PEKE) PE CORP NY.
 XX Venter JC, Adams M, Li PWD, Myers EW;
 PI MPI; 2001-656860/75.
 XX N-PSDB; ABL05842.
 DR
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signaling and cell-cell
 PT interactions.
 PS
 XX Disclosure; SEQ ID NO 12009; 21pp + Sequence Listing; English.
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signaling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA
 CC sequences (AB101840-AB16175) and the encoded proteins (AB57737-
 CC AB572072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 CC
 XX
 SQ Sequence 805 AA;

Query Match 59.7%; Score 40; DB 4; Length 805;
 Best Local Similarity 54.5%; Pred. No. 7.5e+02;
 Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 QY 1 EFAGLVLGGQ 11
 :| |||:| |:
 Db 172 DFGAGLIGCK 182

RESULT 20
 ID ADJ69760 standard; protein; 875 AA.
 XX ADJ69760;
 AC
 XX 06-MAY-2004 (first entry)
 DT
 XX Human heat mitochondrial protein as a therapeutic target Segid1566.
 DE
 XX mitochondrial; human; screening assay; diabetes mellitus;
 KW Huntington's disease; osteoarthritis;
 KW Leber's hereditary optic neuropathy; LHON;
 KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
 KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
 KW neuroprotective; neurotropic; antidiabetic; anticonvulsant; antiarthritic;
 KW osteopathic; ophthalmological; cytostatic.
 KM
 XX
 XX Homo sapiens.
 OS
 XX WO2003087768-A2.
 PN
 XX 23-OCT-2003.
 PD
 XX 04-APR-2003; 2003WO-US010870.
 PF
 XX 12-APR-2002; 2002US-0372843P.
 PR 17-JUN-2002; 2002US-0389987P.
 PR 20-SEP-2002; 2002US-0412418P.
 XX
 XX (MITO-) MITOKOR.
 PA (BUCK-) BUCK INST AGE RES.
 PA

XX Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;
 PI Warnock DE;
 PI MPI; 2003-845369/78.
 DR
 XX
 XX Identifying a mitochondrial target for drug screening assays and for
 PT treating diseases associated with altered mitochondrial function,
 PT comprises detecting a modified polypeptide in a sample and correlating
 PT with the disease.
 PS
 XX Claim 1; SEQ ID NO 1566; 180pp; English.
 CC This invention relates to novel mitochondrial targets that can be used
 CC for therapeutic intervention in treating a disease associated with
 CC altered mitochondrial function. Specifically, it refers to a method for
 CC identifying proteins of the human heart mitochondrial proteome that are
 CC useful for drug screening assays, as well as therapeutic targets. The
 CC present invention describes a method for identifying such proteins that
 CC can be used in the treatment of various diseases associated with altered
 CC mitochondrial function including diabetes mellitus, Huntington's disease,
 CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
 CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
 CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
 CC compositions have neuroprotective, neurotropic, antidiabetic,
 CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and
 CC cytosstatic activities. This polypeptide sequence is a human heart
 CC mitochondrial protein of the invention.
 CC
 XX
 SQ Sequence 875 AA;

Query Match 59.7%; Score 40; DB 7; Length 875;
 Best Local Similarity 54.5%; Pred. No. 8.2e+02;
 Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 QY 1 EFAGLVLGGQ 11
 :| |||:| |:
 Db 169 DFGAGLIGCK 179

RESULT 21
 ID AAY11027 standard; protein; 220 AA.
 XX AAY11027;
 AC
 XX 08-JUN-1999 (first entry)
 DT
 XX H. pylori ORF 029e41622_34176513_c1_50 outer membrane protein.
 DE
 XX Vaccine; probe; diagnostic; ORF; cell envelope protein; secreted protein;
 KW cytoplasmic protein; cellular protein.
 KW
 XX Helicobacter pylori.
 OS
 XX WO9824475-A1.
 PN
 XX 11-JUN-1998.
 PD
 XX 05-DEC-1997; 97WO-US022104.
 PF
 XX 05-DEC-1996; 96US-00759625.
 PR 25-MAR-1997; 97US-00823745.
 PR 14-JUL-1997; 97US-00891928.
 XX
 XX (ASTR) ASTRA AB.
 PA
 XX Smith D, Alm RA, Doig PC, Kabok Z, Castriciotta LM,
 PI WPI; 1998-333051/29.
 DR N-PSDB; AAX30556.
 DR
 XX New isolated Helicobacter pylori nucleic acids - used to develop products
 PT

PT for the diagnosis, prevention and treatment of infection by H. pylori and
PT other Helicobacter species.
XX
PS Claim 37, 41; Page 190; 339pp; English.
CC Recombinant or substantially pure preparations of H. pylori polypeptides
CC are disclosed, together with the nucleic acids encoding them. In all, 97
CC ORFs are shown. The proteins are variously cell envelope proteins,
CC cytoplasmic proteins, secreted proteins or other cellular proteins.
CC Vaccines containing the nucleic acids or proteins are claimed, as are
CC probes containing at least 8 nucleotides from the nucleic acid sequences.
CC The vaccines are useful for treating or reducing the risk of H. pylori
CC infections, and the probes can be used diagnostically for detecting the
CC presence of Helicobacter in a sample. The products are also of use in
CC screening for compounds having the ability to interfere with the H.
CC pylori life cycle or to inhibit H. pylori infection
XX
SQ Sequence 220 AA;
Query Match 58.2%; Score 39; DB 2; Length 220;
Best Local Similarity 63.6%; Pred. No. 2.8e+02;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 3 GAGLVGQGFM 13
| : ||| : | :
Db 70 GFGVVLGSKFV 80
RESULT 22
AAW98208
ID AAW98208 standard; protein; 220 AA.
XX
AC AAW98208;
XX
DT 31-MAR-1999 (first entry)
DE H. pylori GHPO 635 protein.
XX
XX GHPO protein; Helicobacter infection; gastroduodenal disease; gastritis;
KM peptic ulcer disease.
XX
OS Helicobacter pylori.
XX
PN WO9843478-A1.
XX
PD 08-OCT-1998.
XX
PF 01-APR-1998; 98WO-US006371.
XX
PR 01-APR-1997; 97US-00833457.
PR 24-JUN-1997; 97US-00881227.
PR 29-JUL-1997; 97US-00902615.
XX
PA (INNR) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS.
XX (HUMA-) HUMAN GENOME SCI INC.
PI Kleantous H, Al-Garawi A, Miller C, Tomb J, Oomen RP;
XX
XX WPI; 1998-542293/46.
DR N-PSDB; AAX13927.
XX
PT New isolated Helicobacter polynucleotides - used to develop products for
PT the diagnosis, prevention and treatment of Helicobacter infections and
PT gastrointestinal diseases.
XX
PS Claim 8; Page 111-113; 2054pp; English.
XX
CC This sequence represents a Helicobacter pylori GHPO protein of the
CC invention. The polypeptides can be used for preventing or treating
CC Helicobacter infections, and gastroduodenal diseases associated with
CC these infections, including acute, chronic, and atrophic gastritis, and
CC peptic ulcer diseases, e.g. gastric and duodenal ulcers. They can also be
CC used for the production of antibodies. The products can also be used for

CC detection and diagnosis
XX
SQ Sequence 220 AA;
Query Match 58.2%; Score 39; DB 2; Length 220;
Best Local Similarity 63.6%; Pred. No. 2.8e+02;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 3 GAGLVGQGFM 13
| : ||| : | :
Db 70 GFGVVLGSKFV 80
RESULT 23
AA17195
ID AA17195 standard; protein; 220 AA.
XX
AC AA17195;
XX
DT 03-AUG-1999 (first entry)
DE H. pylori outer membrane polypeptide.
XX
XX Outer membrane polypeptide; OMP; vaccine; H. pylori infection; humoral;
KM cellular immune response.
XX
OS Helicobacter pylori.
XX
PN WO921959-A2.
XX
PD 06-MAY-1999.
XX
PF 28-OCT-1998; 98WO-US022883.
XX
PR 28-OCT-1997; 97US-00959131.
PR 17-DEC-1997; 97US-00993001.
XX
XX (GENO-) GENOME THERAPEUTICS CORP.
PA
XX
XX Ellis RW, Noonan BM, Alm RA, Smith D, Guild BC;
PI
XX
XX WPI; 1999-326698/27.
DR N-PSDB; AAX75814.
XX
PT Cellular vaccine against Helicobacter pylori.
XX
PS Claim 7; Page 269-270; 352pp; English.
XX
CC The invention relates to a vaccine for preventing or treating infections
CC by Helicobacter pylori. The vaccine contains at least one isolated H.
CC pylori polypeptide, or its fragments, in a carrier, where the carrier is
CC a Salmonella, Vibrio cholerae or Shigella vector containing a nucleic
CC acid encoding the H. pylori polypeptide. The vaccines induce humoral and
CC cellular immune responses. The vaccines are used to treat or prevent
CC infections by H. pylori. Sequences AAX75779 to AAX75837 represent nucleic
CC acid sequences encoding H. pylori outer membrane polypeptides (OMPs)
CC AA17160 to AA17218
XX
SQ Sequence 220 AA;
Query Match 58.2%; Score 39; DB 2; Length 220;
Best Local Similarity 63.6%; Pred. No. 2.8e+02;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 3 GAGLVGQGFM 13
| : ||| : | :
Db 70 GFGVVLGSKFV 80
RESULT 24
ABU22234
ID ABU22234 standard; protein; 419 AA.
XX

AC AB022234;
 XX
 DT 19-JUN-2003 (first entry)
 XX
 DE Protein encoded by Prokaryotic essential gene #7761.
 XX
 KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
 XX
 OS Burkholderia mallei.
 XX
 PN W0200277183-A2.
 XX
 PD 03-OCT-2002.
 XX
 PF 21-MAR-2002; 2002WO-US009107.
 XX
 PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00948993.
 PR 25-OCT-2001; 2001US-03422923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 XX
 PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX
 DR WPI; 2003-029926/02.
 DR N-PSDB; ACA26104.
 XX
 PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.
 XX
 PS Claim 25; SEQ ID NO 50158; 1766pp; English.
 XX
 CC The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway;
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 419 AA;

Query Match 58.2%; Score 39; DB 6; Length 419;
 Best Local Similarity 61.5%; Pred. No. 5.5e+02;
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EFGAGLVGGQFM 13
 DB 254 EFGAELIDGPFWM 266

RESULT 25
 ADE86082
 ID ADE86082 standard; protein; 450 AA.
 XX
 AC ADE86082;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Streptomyces hygroscopicus efflux protein.
 XX
 KW antibiotic; AC98; efflux protein.
 XX
 OS Streptomyces hygroscopicus.
 XX
 PN W02003082909-A1.
 XX
 PD 09-OCT-2003.
 XX
 PF 28-MAR-2003; 2003WO-US009746.
 PF 29-MAR-2002; 2002US-0368713P.
 XX
 PA (AMHP) WYETH.
 XX
 PI Hucul JA, Macgarvey N, Greenstein M;
 PI WPI; 2003-812536/76.
 DR N-PSDB; ADE86070.
 XX
 PT New non-ribosomal peptide synthetase, useful for preparing antibacterial
 PT peptides, derived from Streptomyces, also related nucleic acid and
 PT modified antibiotics.
 XX
 PS Claim 10; SEQ ID NO 30; 163pp; English.
 XX
 CC The present sequence is the protein sequence of an efflux protein thought
 CC to be involved in the biosynthesis of the peptide antibiotic AC98 of
 CC Streptomyces hygroscopicus NS17 (NRRL 30439). The sequence is predicted
 CC from an open reading frame (ORF10) in a gene cluster ADE86070 isolated
 CC from NS17, which includes a non-ribosomal peptide synthetase (NRPS)
 CC complex. Sequence comparisons of specific ORPs indicated that the encoded
 CC proteins are tailoring enzymes involved in modification of the AC98
 CC peptide core, e.g. glycosylation, methylation or acylation, or in
 CC resistance. The invention provides a method of producing a cyclic
 CC transformed host cells. It also provides a method of producing a cyclic
 CC peptide antibiotic, such as AC98, using the NRPS comprised of mpba
 CC ADE86071 and mpba ADE86072. The antibiotic is preferably a
 CC 11poaglycopeptide antibiotic with activity against Gram-positive
 CC pathogens. Also provided are methods of modifying NRPS to produce an
 CC antibiotic having a modified peptide core, and a method for evaluating
 CC the structural regions of the modified peptide.
 XX
 SQ Sequence 450 AA;

Query Match 58.2%; Score 39; DB 7; Length 450;
 Best Local Similarity 72.7%; Pred. No. 5.9e+02;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 2 EFGAGLVGGQF 12
 DB 305 EFGAGLVGGQF 315

RESULT 26
 ABR53218
 ID ABR53218 standard; protein; 770 AA.
 XX

AC ABR53218;
 XX
 DT 20-JUN-2003 (first entry)
 XX
 DE Protein sequence #SEQ ID 1301.
 XX
 DE Multi-protein complex; eukaryote; drug target; diagnosis.
 XX
 OS Saccharomyces cerevisiae.
 XX
 PN EPI258494-A1.
 XX
 PD 20-NOV-2002.
 XX
 PF 20-DEC-2001; 2001EP-00130253.
 XX
 PR 15-MAY-2001; 2001EP-00111774.
 XX
 PA (CELL-) CELLZOME AG.
 XX
 PI Bauer A, Gavin A, Grandi P, Krause R, Kruse UD, Kuester BD;
 PI Marzloch M, Schultz JD, Superti-Furga G;
 XX
 DR WPI; 2003-250078/25.
 DR N-PSDB; ACC61260.
 XX
 PT New isolated protein complexes useful for diagnosing a disease or
 disorder, or as a target for an active agent of a pharmaceutical,
 PT preferably a drug target in the treatment or prevention of disease or
 disorder.
 PS Disclosure; SEQ ID NO 1301; 17pp + Sequence Listing; English.
 XX
 CC The invention relates to multi-protein complexes from eukaryotes. Proteins
 CC of the invention and DNA sequences encoding them are given in records
 CC ABR53568-ABR53903 and ACC60610-ACC61944 respectively. The complexes are
 CC obtainable by using a protein as a bait and isolating the set of proteins
 CC which is attached thereto from cells. Such protein complexes may comprise
 CC up to 30 distinct proteins. Protein complexes of the invention are useful
 CC for diagnosing a disease or disorder, or as a target for an active agent
 CC of a pharmaceutical, preferably a drug target in the treatment or
 CC prevention of a disease or disorder. Note: The sequence data for this
 CC patent is not represented in the printed specification, but is based on
 CC sequence information supplied by the European Patent Office. The complete
 CC document is available on CD-ROM
 CC
 SQ Sequence 770 AA;
 QY
 Query Match 58.2%; Score 39; DB 6; Length 770;
 Best Local Similarity 70.0%; Pred. No. 1e+03; 1; Indels 0; Gaps 0;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 DB 142 FSGGLVIGGK 151
 QY 2 FSGGLVIGGQ 11
 ID ABR53218
 ID ADK63726 standard; protein; 770 AA.
 XX
 AC ADK63726;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Disease treating protein complex-derived protein #790.
 XX
 KM protein complex; drug target; diagnosis.
 XX
 OS Unidentified.
 XX
 PN EPI338608-A2.
 XX

PD 27-AUG-2003.
 XX
 PF 20-DEC-2002; 2002EP-00102902.
 XX
 PR 20-DEC-2001; 2001EP-00130253.
 XX
 PA (CELL-) CELLZOME AG.
 XX
 PI Bauer A, Gavin A, Superti-Furga G, Kuester B, Schultz J;
 PI Marzloch M, Grandi P, Krause R, Kruse U, Merino A, Bauch A;
 PI Michon A, Leutwein C, Rick J;
 XX
 DR WPI; 2003-638460/61.
 DR N-PSDB; ADK63727.
 XX
 PT New proteins and protein complexes from eukaryotes, useful as targets in
 PT drug screening, or in diagnosing or screening for the presence of a
 PT disease or disorder, or a predisposition for developing a disease or
 PT disorder in a subject.
 PS Disclosure; SEQ ID NO 1579; 13pp; English.
 XX
 CC The invention relates to novel protein complexes comprising a first and a
 CC second protein, or its derivative, fragment, homologue or variant. The
 CC proteins are selected from given protein complexes, which are not defined
 CC in the specification. The variants are encoded by nucleic acids that
 CC hybridize to the nucleic acids encoding the proteins under low stringency
 CC conditions. The protein complexes are useful as targets for an active
 CC agent of a pharmaceutical. These protein complexes are particularly
 CC useful as drug targets for the treatment or preventing of a disease or
 CC disorder. The complexes and methods above are useful in diagnosing or
 CC screening for the presence of a disease or disorder or a predisposition
 CC for developing a disease or disorder in a subject. These are also useful
 CC in screening for a drug for treatment or prevention of a disease or
 CC disorder. The molecule that modulates the amount, activity or protein
 CC components of the complex is useful for the manufacture of a medicament
 CC for the treatment or prevention of a disease or disorder. This sequence
 CC corresponds to a protein of the invention. (Note: the sequence data for
 CC this patent did not form part of the printed specification but was
 CC obtained from the EPO in electronic format).
 CC
 SQ Sequence 770 AA;
 QY
 Query Match 58.2%; Score 39; DB 7; Length 770;
 Best Local Similarity 70.0%; Pred. No. 1e+03; 1; Indels 0; Gaps 0;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 DB 142 FSGGLVIGGK 151
 QY 2 FSGGLVIGGQ 11
 ID ABR53218
 ID ABJ26177 standard; protein; 810 AA.
 XX
 AC ABJ26177;
 XX
 DT 16-APR-2003 (first entry)
 XX
 DE Aspergillus fumigatus essential gene protein #835.
 XX
 KM Fungicide; cytostatic; essential gene; Aspergillus fumigatus; infection;
 KM cancer; contamination; biofilm; antibody; immune response.
 XX
 OS Aspergillus fumigatus.
 XX
 PN WO200286090-A2.
 XX
 PD 31-OCT-2002.
 XX
 PF 23-APR-2002; 2002WO-US013142.
 XX

XX US6551795-B1.
XX 22-APR-2003.
XX 18-FEB-1999; 99US-00252991.
XX 18-FEB-1998; 98US-0074788P.
XX 27-JUL-1998; 98US-0094190P.
XX (GENO-) GENOME THERAPEUTICS CORP.
XX Rubenfield MJ, Nolling J, DeLoughery C, Bush D;
XX MPI: 2003-615309/58.
XX N-PSDB; ABD09802.
XX Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
XX useful as molecular targets for diagnostics, prophylaxis and treatment of
XX pathological conditions resulting from bacterial infection.
XX Disclosure; SEQ ID NO 24977; 455pp; English.
XX The invention relates to Pseudomonas aeruginosa polypeptides and the
XX polymucleotides encoding them. The sequences are useful in diagnosis and
XX therapy of pathological conditions, as molecular targets for diagnostics,
XX prophylaxis and treatment of pathological conditions resulting from a
XX bacterial infection, for evaluating a compound, such as a polypeptide,
XX for the ability to bind a P. aeruginosa nucleic acid, as components of
XX effective antibacterial targets, as targets for antibacterial drugs,
XX including anti-P. aeruginosa drugs, as templates for recombinant
XX production of P. aeruginosa-derived peptides or polypeptides, as target
XX components for diagnosis and/or treatment of P. aeruginosa-caused
XX infection, and in detection of P. aeruginosa sequences or other sequences
XX of Pseudomonas species using biopchip technology. Sequences AB067826-
XX AB084336 represent P. aeruginosa polypeptides of the invention. Note: The
XX sequence data for this patent did not form part of the printed
XX specification but was obtained in electronic format from USPTO at
XX seqdata.uspto.gov/sequence.html
XX SQ Sequence 903 AA;
XX
XX Query Match 57.5%; Score 38.5; DB 7; Length 903;
XX Best Local Similarity 64.3%; Pred. No. 1.5e+03;
XX Matches 9; Conservative 1; Mismatches 1; Indels 3; Gaps 1;
XX
XX 2 FGAG--LVLGQGF 12
XX ||||| |||||
XX 509 FGAGPAAALAGGEF 522
XX
XX RESULT 31
XX AAG35239
XX ID AAG35239 standard; protein; 191 AA.
XX AC AAG35239;
XX 18-OCT-2000 (first entry)
XX Zea maye protein fragment SEQ ID NO: 43019.
XX
XX Protein identification; signal transduction pathway; metabolic pathway;
XX hybridization assay; genetic mapping; gene expression control; promoter;
XX termination sequence; corn.
XX Zea maye subsp. maye.
XX EP1033405-A2.
XX 06-SEP-2000.
XX 25-FEB-2000; 2000EP-00301439.
XX

PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 23-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 06-MAY-1999; 99US-0132487P.
PR 07-MAY-1999; 99US-0132633P.
PR 11-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135333P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142393P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR

PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 17-JUL-1999; 99US-0144086P.
PR 18-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144336P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0145086P.
PR 22-JUL-1999; 99US-0145086P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145226P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145918P.
PR 28-JUL-1999; 99US-0145918P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 03-AUG-1999; 99US-0146389P.
PR 04-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 05-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147312P.
PR 06-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 09-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 10-AUG-1999; 99US-0147935P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148565P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153707P.
PR 13-SEP-1999; 99US-0153788P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.

PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161922P.
PR 28-OCT-1999; 99US-0161933P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 56.7%; Score 38; DB 3; Length 191;
Best Local Similarity 66.7%; Pred. No. 3.5e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 FGAGVILGG 10
Db 74 FGCGVILGG 82

RESULT 32

AGG35238
ID AGG35238 standard; protein; 192 AA.

AC AGG35238;

DT 18-OCT-2000 (first entry)

DE Zea mays protein fragment SEQ ID NO: 43018.

KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence; corn.

XX Zea mays subsp. mays.

OS Zea mays subsp. mays.

PN EPI033405-A2.

PD 06-SEP-2000.

PF 25-FEB-2000; 2000EP-00301439.

XX 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.

PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0128645P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 23-APR-1999; 99US-0130691P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 04-MAY-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 06-MAY-1999; 99US-0132487P.
PR 11-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
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PR 25-MAY-1999; 99US-0136021P.
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RESULT 33

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XX AAG40537;

DT 18-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 50309.

XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.

OS Arabidopsis thaliana.

PN EP1033405-A2.

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Best Local Similarity 66.7%; Pred. No. 3.7e+02;
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DT 17-OCT-2000 (First entry)
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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
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OS Arabidopsis thaliana.
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Query Match 56.7%; Score 38; DB 3; Length 202;
Best Local Similarity 66.7%; Pred. No. 3.7e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 FGAGLVYGG 10
Db 85 FCGGVILGG 93

RESULT 35
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AC
XX 18-OCT-2000 (first entry)
DT
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DE Arabidopsis thaliana protein fragment SEQ ID NO: 50308.
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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
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XX Arabidopsis thaliana.
OS
XX EP1033405-A2.
PN
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PD 06-SEP-2000.
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Query Match 56.7%; Score 38; DB 3; Length 249;
Best local Similarity 66.7%; Pred. No. 4.6e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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Db 132 FGCGTTCG 140
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AC AAG04530;
XX 17-OCT-2000 (first entry)
XX Arabidopsis thaliana protein fragment SEQ ID NO: 590.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 590.
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridization assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX Arabidopsis thaliana.
XX EP1033405-A2.
PN 06-SEP-2000.
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Query Match 56.7%; Score 38; DB 3; Length 249;
Best Local Similarity 66.7%; Pred. No. 4.6e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 FGAGLVIGG 10
Db 132 FGCGVILGG 140

RESULT 37
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XX AAG35237;
AC 18-OCT-2000 (first entry)
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DT
XX
DE Zea mays protein fragment SEQ ID NO: 43017.
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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence; corn.
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XX Zea mays subsp. mays.
PN EP1033405-A2.
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PD 06-SEP-2000.
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PF 25-FEB-2000; 2000EP-00301439.
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 DT 26-MAR-2002 (first entry)
 XX
 DE Drosophila melanogaster polypeptide SEQ ID NO 15657.
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 KM Drosophila; developmental biology; cell signalling; insecticide;
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 OS Drosophila melanogaster.
 XX
 PN WO200171042-A2.
 XX
 PD 27-SEP-2001.
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 PF 23-MAR-2001; 2001MO-US009231.
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 PR 23-MAR-2000; 2000US-0191637P.
 PR 11-JUL-2000; 2000US-00614150.
 XX
 PA (PEKE) PE CORP NY.
 XX
 PI Venter JC, Adams M, Li PWD, Myers EW;
 XX
 DR WPI; 2001-656860/75.
 DR N-PSDB; ABL07058.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions.
 XX
 PS Disclosure; SEQ ID NO 15657; 21bp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (AB16176-AB130511); expressed DNA
 CC sequences (AB101840-AB16175) and the encoded proteins (ABB57737-
 CC ABB72072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
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Seq Sequence 249 AA;
 Query Match 56.7%; Score 38; DB 4; Length 249;
 Best Local Similarity 70.0%; Pred. No. 4.6e+02;
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 DB 92 AGVILGCGLI 101

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 AC ABB65352;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Drosophila melanogaster polypeptide SEQ ID NO 22848.
 XX
 KM Drosophila; developmental biology; cell signalling; insecticide;
 KM pharmaceutical.

XX Drosophila melanogaster.
 OS WO200171042-A2.
 XX 27-SEP-2001.
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 XX 23-MAR-2001; 2001WO-US009231.
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 XX 23-MAR-2000; 2000US-0191637P.
 PR 11-JUL-2000; 2000US-00614150.
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 XX (PEKE) PE CORP NY.
 PA
 XX Venter JC, Adams M, Li FWD, Myers EW;
 PI WPI; 2001-656660/75.
 DR N-PSDB; ABL09455.
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 XX New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signaling and cell-cell
 PT interactions.
 PS Disclosure; SEQ ID NO 22848; 21pp + Sequence listing; English.
 XX
 XX The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signaling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL1840-ABL16175) and the encoded proteins (AB857737-
 CC AB872072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
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 92 AGTATGGQLI 101
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 AC ADN73077;
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 DT 15-JUL-2004 (first entry)
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 XX Thale cress protein upregulated in E2Fa/Dpa expressing plants SeqID 972.
 DE plant; transgenic; E2Fa/Dpa transcription factor; growth regulator;
 KW animal feed product; thale cress; cell wall biosynthesis;
 KW nitrogen metabolism; carbon metabolism.
 XX
 OS Arabidopsis thaliana.
 OS
 PN WO2004035798-A2.
 XX
 XX 29-APR-2004.
 PD
 XX 20-OCT-2003; 2003WO-EP011658.
 PF
 XX 18-OCT-2002; 2002EP-00079408.
 PR
 XX (CROP-) CROPDESTIGN NV.
 PA
 XX

PI Inze D, De Veylder L, Vlieghe K;
 XX WPI; 2004-348466/32.
 DR N-PSDB; ADN73076.
 XX
 XX Altering plant characteristics, useful for producing plants for enzyme or
 PT pharmaceutical production comprises modifying in a plant, expression of
 PT one or more nucleic acids and/or modifying level or activity of one or
 PT more proteins.
 XX
 PS Claim 1; SEQ ID NO 972; 134pp; English.
 XX
 XX This invention relates to a novel method for altering one or more plant
 CC characteristics. Specifically, it refers to identifying genes that are up
 CC - or down-regulated in transgenic plants overexpressing the heterodimeric
 CC E2Fa/Dpa transcription factor of Arabidopsis and using these sequences to
 CC alter plant characteristics accordingly. The present invention describes
 CC generating transgenic plants for the production of growth regulators,
 CC enzymes, therapeutics, pharmaceuticals and animal feed products, where
 CC the altered plant characteristics are selected from increased yield or
 CC biomass, enhanced survival capacity, stress tolerance, plant architecture
 CC or physiology, altered lipid mobilisation and/or altered photosynthesis,
 CC transduction, storage lipid mobilisation and/or altered photosynthesis,
 CC each relative to the corresponding wild type plants. Accordingly, these
 CC sequences can also be useful as positive or negative selectable markers
 CC during transformation of cells or tissues. The identified genes play a
 CC role in a variety of biological processes such as DNA replication, cell
 CC wall biosynthesis, nitrogen and/or carbon metabolism or they function as
 CC transcription factors. This polypeptide sequence is thale cress protein
 CC expressed by a gene upregulated 1.3 fold or more in plants overexpressing
 CC the E2Fa/Dpa transcription factor, given in an exemplification of the
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 OY Query Match 56.7%; Score 38; DB 8; Length 249;
 DB Best Local Similarity 66.7%; Pred. No. 4.6e+02;
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 2 FGAGTATGG 10
 132 FGCGTATGG 140
 Search completed: December 9, 2004, 09:16:30
 Job time : 9.05036 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 9, 2004, 09:21:02 ; Search time 4.58273 Seconds
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Title: US-09-462-416-1
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Searched: 1585576 seqs, 357178320 residues

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	41	61.2	319	14	US-10-156-761-9015 Sequence 9015, Ap
5	40	59.7	875	16	US-10-408-765A-1566 Sequence 1566, Ap
6	39	58.2	178	15	US-10-335-977-5090 Sequence 5090, Ap
7	39	58.2	220	9	US-09-881-752A-16 Sequence 16, Appl
8	39	58.2	220	15	US-10-335-977-5091 Sequence 5091, Ap
9	39	58.2	403	15	US-10-425-114-48433 Sequence 48433, A
10	39	58.2	405	15	US-10-425-114-41675 Sequence 41675, A
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ALIGNMENTS

RESULT 1
US-10-425-115-267639
; Sequence 267639, Application US/10425115
; General Information: US20040214272A1
; Applicant: La Rosa, Thomas J.
; Applicant: Kovalic, David K.
; Applicant: Zhou, Yihua
; Title of Invention: Nucleic Acid Molecules and Other Molecules Associated With
; File Reference: 38-21(53222)B
; Current Application Number: US/10/425,115
; Current Filing Date: 2003-04-28
; Number of SEQ ID NOS: 369326
; SEQ ID NO 267639
; Length: 123
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; Organism: Zea mays
; Feature:
; Other Information: Clone ID: MRT4577_175692C.1.dep
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Db 36 DYSGSLVIGGQ 46

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; Sequence 197757, Application US/10424599
; Publication No. US20040031072A1

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; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT FILING DATE: 2003-04-28
; CURRENT APPLICATION NUMBER: US/10/424,599
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 19757
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Glycine max
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; OTHER INFORMATION: Clone ID: PAT_MRT3847_205C.1.pep
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; Sequence 27, Application US/10041018
; Publication No. US20040072323A1
; GENERAL INFORMATION:
; APPLICANT: Matsuda, Seiichi P.T.
; APPLICANT: Hart, Elizabeth A.
; TITLE OF INVENTION: Diterpene-Producing Unicellular Organism
; FILE REFERENCE: P02080US1/10023547
; CURRENT APPLICATION NUMBER: US/10/041,018
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: US 60/259880
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 291
; TYPE: PRT
; ORGANISM: Chlamydia trachomatis
US-10-041-018-27

```

```

Query Match      61.2% Score 41; DB 15; Length 291;
Best Local Similarity 63.6%; Pred. No. 1.5e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      2 FGAAGLVGGQF 12
      |||||
      153 FGVGGILGGQY 163

```

```

RESULT 4
US-10-156-761-9015
; Sequence 9015, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: HORIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIRA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761

```

```

; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 9015
; LENGTH: 319
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-9015

```

```

Query Match      61.2% Score 41; DB 14; Length 319;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      3 GAGLVGGQ 11
      |||||
      143 GGGVLGGQ 151

```

```

RESULT 5
US-10-408-765A-1566
; Sequence 1566, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Brian D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Martock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1566
; LENGTH: 875
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-1566

```

```

Query Match      59.7% Score 40; DB 16; Length 875;
Best Local Similarity 54.5%; Pred. No. 6.5e+02;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      1 FGAAGLVGGQ 11
      |||||
      169 FGAAGLVGGQ 179

```

```

RESULT 6
US-10-335-977-5090
; Sequence 5090, Application US/10335977
; Publication No. US20040052799A1
; GENERAL INFORMATION:
; APPLICANT: DOUGLAS SMITH et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; RELATING TO HELICOBACTER PYLORI FOR
; DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 10031
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:

```

MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT 4.0
SOFTWARE: UNIX
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN-018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 5090:
SEQUENCE CHARACTERISTICS:
LENGTH: 178 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Helicobacter pylori
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...178
SEQUENCE DESCRIPTION: SEQ ID NO: 5090:
US-10-335-977-5090

Query Match 58.2%; Score 39; DB 15; Length 178;
Best Local Similarity 63.6%; Pred. No. 1.8e+02;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
Qy 3 GAGLVGQPM 13
Db 28 GFGVVGKRV 38

RESULT 7
US-09-881-752A-16
Sequence 16, Application US/09881752A
Patent No. US20020115078A1
GENERAL INFORMATION:
APPLICANT: Kleantous, Harold
APPLICANT: Al-Garawi, Amal
APPLICANT: Miller, Charles
APPLICANT: Tomb, Jean-Francois
APPLICANT: Oomen, Raymond P.
TITLE OF INVENTION: Identification of Polynucleotides
TITLE OF INVENTION: Encoding No. US20020115078A1 Helicobacter Polypeptides in the
FILE REFERENCE: 06132/041002
CURRENT APPLICATION NUMBER: US/09/881,752A
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 08/833,457
PRIOR FILING DATE: 1997-04-01
NUMBER OF SEQ ID NOS: 370
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 16
LENGTH: 220
TYPE: PRT
ORGANISM: Helicobacter pylori
US-09-881-752A-16

Query Match 58.2%; Score 39; DB 9; Length 220;
Best Local Similarity 63.6%; Pred. No. 2.3e+02;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
Qy 3 GAGLVGQPM 13
Db 13 GAGLVGQPM 13

Db 70 GFGVVGKRV 80

RESULT 8
US-10-335-977-5091
Sequence 5091, Application US/10335977
Publication No. US20040052799A1
GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
RELATING TO HELICOBACTER PYLORI FOR
DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 10031
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT 4.0
SOFTWARE: UNIX
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN-018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 5091:
SEQUENCE CHARACTERISTICS:
LENGTH: 220 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Helicobacter pylori
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...220
SEQUENCE DESCRIPTION: SEQ ID NO: 5091:
US-10-335-977-5091

Query Match 58.2%; Score 39; DB 15; Length 220;
Best Local Similarity 63.6%; Pred. No. 2.3e+02;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
Qy 3 GAGLVGQPM 13
Db 70 GFGVVGKRV 80

RESULT 9
US-10-425-114-4843
Sequence 4843, Application US/10425114
Publication No. US2004003488A1
GENERAL INFORMATION:
APPLICANT: Liu, Jindong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E.
APPLICANT: Tabaska, Jack E.
APPLICANT: Cao, Yongwei

```

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 48433
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3068-059-A10_FLI.pep
US-10-425-114-48433
```

```

Query Match          58.2%; Score 39; DB 15; Length 403;
Best Local Similarity 53.8%; Pred. No. 4.3e+02;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      1  EFGAGLVGGQFM 13
Db      152 DVGAGLVGGDL 164
```

```

RESULT 10
US-10-425-114-41675
; Sequence 41675, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 41675
; LENGTH: 405
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB143-006-F6_FLI.pep
US-10-425-114-41675
```

```

Query Match          58.2%; Score 39; DB 15; Length 405;
Best Local Similarity 53.8%; Pred. No. 4.3e+02;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      1  EFGAGLVGGQFM 13
Db      150 DVGAGLVGGDL 162
```

```

RESULT 11
US-10-425-114-48462
; Sequence 48462, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
```

```

; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 48462
; LENGTH: 405
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3060-100-A6_FLI.pep
US-10-425-114-48462
```

```

Query Match          58.2%; Score 39; DB 15; Length 405;
Best Local Similarity 53.8%; Pred. No. 4.3e+02;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      1  EFGAGLVGGQFM 13
Db      150 DVGAGLVGGDL 162
```

```

RESULT 12
US-10-425-114-49554
; Sequence 49554, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 49554
; LENGTH: 405
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3689-213-B12_FLI.pep
US-10-425-114-49554
```

```

Query Match          58.2%; Score 39; DB 15; Length 405;
Best Local Similarity 53.8%; Pred. No. 4.3e+02;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      1  EFGAGLVGGQFM 13
Db      150 DVGAGLVGGDL 162
```

```

RESULT 13
US-10-282-122A-50158
; Sequence 50158, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zykkind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA_034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
```

PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PAM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patent version 3.1
SEQ ID NO 50158
LENGTH: 419
TYPE: PRT
ORGANISM: Burkholderia mallei
US-10-282-122A-50158

Query Match 58.2%; Score 39; DB 14; Length 419;
Best Local Similarity 61.5%; Pred. No. 4.4e+02;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EFGAGLVGGQFM 13
DB 254 EFGAGLVGGQFM 266

RESULT 14
US-10-402-842-30
Sequence 30, Application US/10402842
Publication No. US20030219872A1
GENERAL INFORMATION:
APPLICANT: Magarvey, Nathan A.
APPLICANT: Hucul, John A.
TITLE OF INVENTION: NON-RIBOSOMAL PEPTIDE SYNTHETASES AND ASSOCIATED BIOSYNTHETIC GEN
FILE REFERENCE: 0630/10854-US1
CURRENT APPLICATION NUMBER: US/10/402,842
CURRENT FILING DATE: 2003-03-28
PRIOR APPLICATION NUMBER: US 60/368,713
PRIOR FILING DATE: 2002-03-30
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patent version 3.1
SEQ ID NO 30
LENGTH: 450
TYPE: PRT
ORGANISM: Streptomyces hygroscopicus
US-10-402-842-30

Query Match 58.2%; Score 39; DB 14; Length 450;
Best Local Similarity 72.7%; Pred. No. 4.8e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 FGAAGLVGGQF 12
DB 305 FGAAGLVGGQF 315

RESULT 15
US-10-369-493-21791
Sequence 21791, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:

APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 21791
LENGTH: 528
TYPE: PRT
ORGANISM: Rhodobacter capsulatus
US-10-369-493-21791

Query Match 58.2%; Score 39; DB 14; Length 528;
Best Local Similarity 66.7%; Pred. No. 5.6e+02;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 EFGAGLVGGQF 12
DB 263 EFGAGLVGGQF 274

RESULT 16
US-10-156-761-11459
Sequence 11459, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMTA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 11459
LENGTH: 545
TYPE: PRT
ORGANISM: Streptomyces avermitilis
US-10-156-761-11459

Query Match 58.2%; Score 39; DB 14; Length 545;
Best Local Similarity 70.0%; Pred. No. 5.8e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 AGLVGGQFM 13
DB 332 AGLVGGQFM 341

RESULT 17
US-10-369-493-3245
Sequence 3245, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.

```
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT FILING DATE: 2003-02-28
CURRENT APPLICATION NUMBER: US/10/369,493
PRIOR FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: US 60/360,039
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 3245
LENGTH: 748
TYPE: PRT
ORGANISM: Neurospora crassa
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(748)
OTHER INFORMATION: unsure at all Xaa locations
US-10-369-493-3245
```

```
Query Match          58.2%; Score 39; DB 14; Length 748;
Best Local Similarity 70.0%; Pred. No. 8e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      2 FGAGLVIGGQ 11
        |||||:|:|:|
Db      111 FSAGLVIGGK 120
```

```
RESULT 18
US-10-369-493-22168
Sequence 22168, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT FILING DATE: 2003-02-28
CURRENT APPLICATION NUMBER: US/10/369,493
PRIOR FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: US 60/360,039
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 22168
LENGTH: 770
TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
US-10-369-493-22168
```

```
Query Match          58.2%; Score 39; DB 14; Length 770;
Best Local Similarity 70.0%; Pred. No. 8.3e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      2 FGAGLVIGGQ 11
        |||||:|:|:|
Db      142 FSAGLVIGGK 151
```

```
RESULT 19
US-10-128-714-8235
Sequence 8235, Application US/10128714
Publication No. US20030119013A1
GENERAL INFORMATION:
APPLICANT: Jiang, Bo
APPLICANT: Hu, Wengdi
APPLICANT: Tishkoff, Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Eroszhkin, Alexey M
APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
```

```
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: 10182-018-999
CURRENT APPLICATION NUMBER: US/10/128,714
CURRENT FILING DATE: 2002-04-23
PRIOR FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: US 60/316,362
PRIOR FILING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 8603
SOFTWARE: PatentIn version 3.1
SEQ ID NO 8235
LENGTH: 810
TYPE: PRT
ORGANISM: Aspergillus fumigatus
US-10-128-714-8235
```

```
Query Match          58.2%; Score 39; DB 14; Length 810;
Best Local Similarity 70.0%; Pred. No. 8.7e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      2 FGAGLVIGGQ 11
        |||||:|:|:|
Db      148 FSAGLVIGGK 157
```

```
RESULT 20
US-10-128-714-3235
Sequence 3235, Application US/10128714
Publication No. US20030119013A1
GENERAL INFORMATION:
APPLICANT: Jiang, Bo
APPLICANT: Hu, Wengdi
APPLICANT: Tishkoff, Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Eroszhkin, Alexey M
APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: 10182-018-999
CURRENT APPLICATION NUMBER: US/10/128,714
CURRENT FILING DATE: 2002-04-23
PRIOR FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: US 60/316,362
PRIOR FILING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 8603
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3235
LENGTH: 811
TYPE: PRT
ORGANISM: Aspergillus fumigatus
US-10-128-714-3235
```

```
Query Match          58.2%; Score 39; DB 14; Length 811;
Best Local Similarity 70.0%; Pred. No. 8.7e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      2 FGAGLVIGGQ 11
        |||||:|:|:|
Db      148 FSAGLVIGGK 157
```

```
RESULT 21
US-10-424-599-231652
; Sequence 231652, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 231652
; LENGTH: 94
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(94)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_51202C.1.pep
US-10-424-599-231652
```

```
Query Match          56.7%; Score 38; DB 15; Length 94;
Best Local Similarity 63.6%; Pred. No. 1.4e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      2 FGAGLVGGGF 12
Db      26 FGATLLGGAF 36
```

```
RESULT 22
US-10-425-115-365962
; Sequence 365962, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 365962
; LENGTH: 94
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_96923C.1.pep
US-10-425-115-365962
```

```
Query Match          56.7%; Score 38; DB 17; Length 94;
Best Local Similarity 54.5%; Pred. No. 1.4e+02;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      3 GAGLVGGGFM 13
Db      69 GSHLLIGGFL 79
```

```
RESULT 23
US-10-425-115-294011
; Sequence 294011, Application US/10425115
; Publication No. US20040214272A1
```

```
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 294011
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_31222C.1.pep
US-10-425-115-294011
```

```
Query Match          56.7%; Score 38; DB 17; Length 102;
Best Local Similarity 77.8%; Pred. No. 1.5e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      2 FGAGLVGG 10
Db      93 FGAGIVRG 101
```

```
RESULT 24
US-10-369-493-2228
; Sequence 2228, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 2228
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Schizosaccharomyces pombe
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(146)
; OTHER INFORMATION: unsure at all Xaa locations
US-10-369-493-2228
```

```
Query Match          56.7%; Score 38; DB 14; Length 146;
Best Local Similarity 60.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      2 FGAGLVGG 11
Db      58 FGATLLAG 67
```

```
RESULT 25
US-10-425-115-227826
; Sequence 227826, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
```

```

; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 227826
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_139373C.1.pep
US-10-425-115-227826

Query Match          56.7%; Score 38; DB 17; Length 182;
Best Local Similarity 70.0%; Pred. No. 2.7e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1  EFGAGVLVGG 10
      |||:|
Db      94  EFGSGQALGG 103

RESULT 26
US-10-437-963-203753
; Sequence 203753, Application US/10437963
; Publication No. US2004012343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 203753
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_98906C.1.pep
US-10-437-963-203753

Query Match          56.7%; Score 38; DB 16; Length 238;
Best Local Similarity 70.0%; Pred. No. 3.6e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1  EFGAGVLVGG 10
      |||:|
Db      184  EFGSGQALGG 193

RESULT 27
US-10-425-114-46558
; Sequence 46558, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven B
; APPLICANT: Tabaka, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
```

```

; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 46558
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700352025_FLI.pep
US-10-425-114-46558

Query Match          56.7%; Score 38; DB 15; Length 241;
Best Local Similarity 66.7%; Pred. No. 3.7e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      2  FGAGVLVGG 10
      |||:|
Db      124  FGCGVILGG 132

RESULT 28
US-10-424-599-205502
; Sequence 205502, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 205502
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_27597C.1.pep
US-10-424-599-205502

Query Match          56.7%; Score 38; DB 15; Length 249;
Best Local Similarity 66.7%; Pred. No. 3.8e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      2  FGAGVLVGG 10
      |||:|
Db      132  FGCGVILGG 140

RESULT 29
US-10-437-963-174772
; Sequence 174772, Application US/10437963
; Publication No. US2004012343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 174772
```


LENGTH: 249
TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_72682C.1.pep
US-10-437-963-174772

Query Match
Best Local Similarity 56.7%; Score 38; DB 16; Length 249;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 FGAGLVGG 10
DB 132 FCGGVILGG 140

RESULT 30
US-10-425-115-231962
Sequence 231962, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 231962
LENGTH: 249
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_143142C.1.pep
US-10-425-115-231962

Query Match
Best Local Similarity 56.7%; Score 38; DB 17; Length 249;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 FGAGLVGG 10
DB 132 FCGGVILGG 140

RESULT 31
US-10-425-115-231963
Sequence 231963, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 231963
LENGTH: 249
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_143143C.1.pep
US-10-425-115-231963

Query Match
Best Local Similarity 56.7%; Score 38; DB 17; Length 249;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 2 FGAGLVGG 10
DB 132 FCGGVILGG 140

RESULT 32
US-10-425-115-283162
Sequence 283162, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 283162
LENGTH: 249
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_21341C.1.pep
US-10-425-115-283162

Query Match
Best Local Similarity 56.7%; Score 38; DB 17; Length 249;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 FGAGLVGG 10
DB 132 FCGGVILGG 140

RESULT 33
US-10-425-115-283165
Sequence 283165, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 283165
LENGTH: 249
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_21344C.1.pep
US-10-425-115-283165

Query Match
Best Local Similarity 56.7%; Score 38; DB 17; Length 249;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 FGAGLVGG 10
DB 132 FCGGVILGG 140

RESULT 34
US-10-425-115-283167

```
; Sequence 283167, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 283167
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(249)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_21346C.1.pcp
; US-10-425-115-283167
```

```
Query Match      56.7%; Score 38; DB 17; Length 249;
Best Local Similarity 66.7%; Pred. No. 3.8e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      2 FGAGLVIGG 10
Db      132 FGCGLVIGG 140
```

```
RESULT 35
US-10-425-115-283173
; Sequence 283173, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 283173
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_21351C.1.pcp
; US-10-425-115-283173
```

```
Query Match      56.7%; Score 38; DB 17; Length 249;
Best Local Similarity 66.7%; Pred. No. 3.8e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      2 FGAGLVIGG 10
Db      132 FGCGLVIGG 140
```

```
RESULT 36
US-10-425-115-284033
; Sequence 284033, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
```

```
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 284033
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_22138C.1.pcp
; US-10-425-115-284033
```

```
Query Match      56.7%; Score 38; DB 17; Length 249;
Best Local Similarity 66.7%; Pred. No. 3.8e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      2 FGAGLVIGG 10
Db      132 FGCGLVIGG 140
```

```
RESULT 37
US-10-739-930-7930
; Sequence 7930, Application US/10739930
; Publication No. US20040216190A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; FILE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53377)B
; CURRENT APPLICATION NUMBER: US/10/739,930
; CURRENT FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 11088
; SEQ ID NO 7930
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: ZEMMA-23APR03-C3166_22.p
; US-10-739-930-7930
```

```
Query Match      56.7%; Score 38; DB 17; Length 249;
Best Local Similarity 66.7%; Pred. No. 3.8e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      2 FGAGLVIGG 10
Db      132 FGCGLVIGG 140
```

```
RESULT 38
US-10-424-599-205503
; Sequence 205503, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 205503
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Glycine max
```

```
FEATURE:
NAME/KEY: unsure
LOCATION: (1)-(1256)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_27598C.1.pep
US-10-424-599-205503
```

```
Query Match
Best Local Similarity 56.7%; Score 38; DB 15; Length 256;
Pred. No. 3.9e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 2 FGAGLVLG 10
DB 139 FCGVILGG 147
```

```
RESULT 39
US-10-437-963-174771
Sequence 174771, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 174771
LENGTH: 257
TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_72681C.1.pep
US-10-437-963-174771
```

```
Query Match
Best Local Similarity 56.7%; Score 38; DB 16; Length 257;
Pred. No. 3.9e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 2 FGAGLVLG 10
DB 140 FCGVILGG 148
```

```
RESULT 40
US-10-425-114-41579
Sequence 41579, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jindong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 41579
LENGTH: 259
TYPE: PRT
```

```
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: LIB3078-037-C4_FLI.pep
US-10-425-114-41579
```

```
Query Match
Best Local Similarity 56.7%; Score 38; DB 15; Length 259;
Pred. No. 3.9e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 2 FGAGLVLG 10
DB 142 FCGVILGG 150
```

```
Search completed: December 9, 2004, 09:37:49
Job time : 5.58273 secs
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Db      121 CFFKSPLSNVVCMGGRSTPSLTTKAVLLVRFKQNSPAEDFOBPCCYQSQESQFSCQLAV 180
Qy      181 PEGDSSFYIYSCVAVSSVGSKFSKTQTFQCCGILQDPDPANITVTVAANPRMLSTWOD 240
Db      181 PEGDSSFYIYSCVAVSSVGSKFSKTQTFQCCGILQDPDPANITVTVAANPRMLSTWOD 240
Qy      241 PHSNNSFFYLRFELRYRARSKTFTTMMVKDLOHHCVIDAMSGLRHVVQJLAQEEFQ 300
Db      241 PHSNNSFFYLRFELRYRARSKTFTTMMVKDLOHHCVIDAMSGLRHVVQJLAQEEFQ 300
Qy      301 GEMSEMSPEAMGTPTWTSRSPPAENESTPMQALTTNKDDNLLFRDSANATSLPVEFMP 360
Db      301 GEMSEMSPEAMGTPTWTSRSPPAENESTPMQALTTNKDDNLLFRDSANATSLPVEFMP 357
Qy      361 VPPEGDSKDVAAHPROPLTSSERIDQIRYILDGISAIRKETCNKSMCE--SSKEALAE 418
Db      358 -----DAGEP-----KSCDKHTTCCPCAPPELLGG 382
Qy      419 NNLLNLPKMAEKDGCFOGAFNEETLVKIIIT---GLFEFVYLEYLQ---NRPESSEORAR 472
Db      383 PSVFLPFPKPDOTLMISRTPEVTCVVVDVSHEDPEVFNNYVDGVEVHNAKTKRREOYN 442
Qy      473 AVQMSKTVL 481
Db      443 STYRVVSVL 451

```

RESULT 2

```

US-09-935-868-8
; Sequence 8, Application US/09935868
; Patent No. US20020164590A1
; GENERAL INFORMATION:
; APPLICANT: Regeneron Pharmaceuticals, Inc
; TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using
; FILE REFERENCE: REG 203D
; CURRENT APPLICATION NUMBER: US/09/935,868
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-868-8

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Query Match      67.1%; Score 1921; DB 9; Length 592;
Best Local Similarity 77.1%; Pred. No. 3,7e-140;
Matches 377; Conservative 22; Mismatches 44; Indels 46; Gaps 5;

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Qy      1 MVAVGCALLAALIAFGAALAPRCPAOFVARGVLTSLPGDSVTLTCGVEPEDNATVHM 60
Db      1 MVAVGCALLAALIAFGAALAPRCPAOFVARGVLTSLPGDSVTLTCGVEPEDNATVHM 60
Qy      61 VLRKPAAGSHPSRWAGMGRLLRSVQLHDSGNVSCYRAGRAGTYVHLVDVPEEPQIS 120
Db      61 VLRKPAAGSHPSRWAGMGRLLRSVQLHDSGNVSCYRAGRAGTYVHLVDVPEEPQIS 120
Qy      121 CFFKSPLSNVVCMGGRSTPSLTTKAVLLVRFKQNSPAEDFOBPCCYQSQESQFSCQLAV 180
Db      121 CFFKSPLSNVVCMGGRSTPSLTTKAVLLVRFKQNSPAEDFOBPCCYQSQESQFSCQLAV 180
Qy      181 PEGDSSFYIYSCVAVSSVGSKFSKTQTFQCCGILQDPDPANITVTVAANPRMLSTWOD 240
Db      181 PEGDSSFYIYSCVAVSSVGSKFSKTQTFQCCGILQDPDPANITVTVAANPRMLSTWOD 240
Qy      241 PHSNNSFFYLRFELRYRARSKTFTTMMVKDLOHHCVIDAMSGLRHVVQJLAQEEFQ 300
Db      241 PHSNNSFFYLRFELRYRARSKTFTTMMVKDLOHHCVIDAMSGLRHVVQJLAQEEFQ 300
Qy      301 GEMSEMSPEAMGTPTWTSRSPPAENESTPMQALTTNKDDNLLFRDSANATSLPVEFMP 360

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Db      301 GEMSEMSPEAMGTPTWTSRSPPAENESTPMQALTTNKDDNLLFRDSANATSLPVEFMP 357
Qy      361 VPPEGDSKDVAAHPROPLTSSERIDQIRYILDGISAIRKETCNKSMCE--SSKEALAE 418
Db      358 -----DAGEP-----KSCDKHTTCCPCAPPELLGG 382
Qy      419 NNLLNLPKMAEKDGCFOGAFNEETLVKIIIT---GLFEFVYLEYLQ---NRPESSEORAR 472
Db      383 PSVFLPFPKPDOTLMISRTPEVTCVVVDVSHEDPEVFNNYVDGVEVHNAKTKRREOYN 442
Qy      473 AVQMSKTVL 481
Db      443 STYRVVSVL 451

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RESULT 3

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US-10-287-035-8
; Sequence 8, Application US/10287035
; Publication No. US20030104567A1
; GENERAL INFORMATION:
; APPLICANT: Neil Stahl and George D. Yancopoulos
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: AND USING
; CURRENT APPLICATION NUMBER: US/10/287,035
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: USSN 09/935,868
; PRIOR FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: USSN 09/787,835
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: USSN 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-287-035-8

```

```

Query Match      67.1%; Score 1921; DB 14; Length 592;
Best Local Similarity 77.1%; Pred. No. 3,7e-140;
Matches 377; Conservative 22; Mismatches 44; Indels 46; Gaps 5;

```

```

Qy      1 MVAVGCALLAALIAFGAALAPRCPAOFVARGVLTSLPGDSVTLTCGVEPEDNATVHM 60
Db      1 MVAVGCALLAALIAFGAALAPRCPAOFVARGVLTSLPGDSVTLTCGVEPEDNATVHM 60
Qy      61 VLRKPAAGSHPSRWAGMGRLLRSVQLHDSGNVSCYRAGRAGTYVHLVDVPEEPQIS 120
Db      61 VLRKPAAGSHPSRWAGMGRLLRSVQLHDSGNVSCYRAGRAGTYVHLVDVPEEPQIS 120
Qy      121 CFFKSPLSNVVCMGGRSTPSLTTKAVLLVRFKQNSPAEDFOBPCCYQSQESQFSCQLAV 180
Db      121 CFFKSPLSNVVCMGGRSTPSLTTKAVLLVRFKQNSPAEDFOBPCCYQSQESQFSCQLAV 180
Qy      181 PEGDSSFYIYSCVAVSSVGSKFSKTQTFQCCGILQDPDPANITVTVAANPRMLSTWOD 240
Db      181 PEGDSSFYIYSCVAVSSVGSKFSKTQTFQCCGILQDPDPANITVTVAANPRMLSTWOD 240
Qy      241 PHSNNSFFYLRFELRYRARSKTFTTMMVKDLOHHCVIDAMSGLRHVVQJLAQEEFQ 300
Db      241 PHSNNSFFYLRFELRYRARSKTFTTMMVKDLOHHCVIDAMSGLRHVVQJLAQEEFQ 300
Qy      301 GEMSEMSPEAMGTPTWTSRSPPAENESTPMQALTTNKDDNLLFRDSANATSLPVEFMP 360
Db      301 GEMSEMSPEAMGTPTWTSRSPPAENESTPMQALTTNKDDNLLFRDSANATSLPVEFMP 357

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Qy 361 VPEGDSKDVAAAPHROPLTSSERIDKQIRYILDGIALRKETCKNSMCE--SSKEALAE 418
 Db 358 -----DAGE-----KSCDKHTHCPCPAPRLDGG 382
 Qy 419 NNILNLPKMAKCGCFOSGNETCTLVKIIIT---GLLEFEVYLEYLO---NREBSSEQAR 472
 Db 383 PSVFLEPPPKPDKTLMISRTPEVTCVVDVSHEDPEVKFMVYDGVVHNAKTPFREEQYN 442
 Qy 473 AVQMSTKVL 481
 Db 443 STYRVSVTL 451

RESULT 4

US-10-282-162-8
 ; Sequence 8, Application US/10282162
 ; Publication No. US20030143697A1
 ; GENERAL INFORMATION:
 ; APPLICANT: REGENERON PHARMACEUTICALS, INC.
 ; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
 ; TITLE OF INVENTION: AND USING
 ; FILE REFERENCE: REG 203-B-US
 ; CURRENT APPLICATION NUMBER: US/10/282,162
 ; CURRENT FILING DATE: 2002-10-28
 ; PRIOR APPLICATION NUMBER: 09/787,835
 ; PRIOR FILING DATE: 1999-09-22
 ; PRIOR APPLICATION NUMBER: PCT/US99/22045
 ; PRIOR FILING DATE: 1999-09-22
 ; NUMBER OF SEQ ID NOS: 56
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 8
 ; LENGTH: 592
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-282-162-8

Query Match 67.1%; Score 1921; DB 14; Length 592;

Best Local Similarity 77.1%; Pred. No. 3,7e-140;
 Matches 377; Conservative 22; Mismatches 44; Indels 46; Gaps 5;

Qy 1 MLAVGALLAALLAALPAAALPARRCPAQBVARGVLTSLPGDSVTLTCCPGVEPEDNATVHM 60
 Db 1 MVAVGALLAALLAALPAAALPARRCPAQBVARGVLTSLPGDSVTLTCCPGVEPEDNATVHM 60
 Qy 61 VLRKPAAGSHPRMAGMRLLRSVQLHDSGNVSCYRAGRAGTVHLLVDVPEEPOLLS 120
 Db 61 VLRKPAAGSHPRMAGMRLLRSVQLHDSGNVSCYRAGRAGTVHLLVDVPEEPOLLS 120
 Qy 121 CFRKSPLSNVVCEWGRSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYSGESQKFSQCLAV 180
 Db 121 CFRKSPLSNVVCEWGRSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYSGESQKFSQCLAV 180
 Qy 181 PEGDSSFYIVSMCVASSVSGSKFSKTQTFQCGILOPDPANITVTVAANPRMLSTVWOD 240
 Db 181 PEGDSSFYIVSMCVASSVSGSKFSKTQTFQCGILOPDPANITVTVAANPRMLSTVWOD 240
 Qy 241 PHSWNSFYRLRPELRARERKFTTMMVKDLOHHCVIHDAMSGLRHVQLRAOEFGQ 300
 Db 241 PHSWNSFYRLRPELRARERKFTTMMVKDLOHHCVIHDAMSGLRHVQLRAOEFGQ 300
 Qy 301 GEMSEWSPAMGTPMTESRSPPAENEVSTPMQALTTNKDDNLLFRDSANATSLPVEFMP 360
 Db 301 GEMSEWSPAMGTPMTESRSPPAENEVSTPMQALTTNKDDNLLFRDSANATSLPVEFMP 360
 Qy 361 VPEGDSKDVAAAPHROPLTSSERIDKQIRYILDGIALRKETCKNSMCE--SSKEALAE 418
 Db 358 -----DAGE-----KSCDKHTHCPCPAPRLDGG 382
 Qy 419 NNILNLPKMAKCGCFOSGNETCTLVKIIIT---GLLEFEVYLEYLO---NREBSSEQAR 472
 Db 383 PSVFLEPPPKPDKTLMISRTPEVTCVVDVSHEDPEVKFMVYDGVVHNAKTPFREEQYN 442
 Qy 473 AVQMSTKVL 481

Db 443 STYRVSVTL 451

RESULT 5

US-10-247-463-12
 ; Sequence 12, Application US/10247463
 ; Publication No. US20030082734A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dowling, Lynette M.
 ; APPLICANT: Timans, Jacqueline C.
 ; APPLICANT: Gorman, Daniel M.
 ; APPLICANT: Kastelein, Robert A.
 ; APPLICANT: Bazan, J. Fernando
 ; TITLE OF INVENTION: Mammalian Receptor Proteins; Related Reagents and
 ; TITLE OF INVENTION: Methods
 ; FILE REFERENCE: DX09920
 ; CURRENT APPLICATION NUMBER: US/10/247,463
 ; CURRENT FILING DATE: 2002-09-18
 ; PRIOR APPLICATION NUMBER: US/09/588,113
 ; PRIOR FILING DATE: 2000-05-31
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 12
 ; LENGTH: 468
 ; TYPE: PRT
 ; ORGANISM: primate
 ; US-10-247-463-12

Query Match 67.0%; Score 1918; DB 14; Length 468;

Best Local Similarity 96.5%; Pred. No. 4.6e-140;
 Matches 360; Conservative 1; Mismatches 4; Indels 8; Gaps 1;

Qy 1 MLAVGALLAALLAALPAAALPARRCPAQBVARGVLTSLPGDSVTLTCCPGVEPEDNATVHM 60
 Db 1 MVAVGALLAALLAALPAAALPARRCPAQBVARGVLTSLPGDSVTLTCCPGVEPEDNATVHM 60
 Qy 61 VLRKPAAGSHPRMAGMRLLRSVQLHDSGNVSCYRAGRAGTVHLLVDVPEEPOLLS 120
 Db 61 VLRKPAAGSHPRMAGMRLLRSVQLHDSGNVSCYRAGRAGTVHLLVDVPEEPOLLS 120
 Qy 121 CFRKSPLSNVVCEWGRSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYSGESQKFSQCLAV 180
 Db 121 CFRKSPLSNVVCEWGRSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYSGESQKFSQCLAV 180
 Qy 181 PEGDSSFYIVSMCVASSVSGSKFSKTQTFQCGILOPDPANITVTVAANPRMLSTVWOD 240
 Db 181 PEGDSSFYIVSMCVASSVSGSKFSKTQTFQCGILOPDPANITVTVAANPRMLSTVWOD 240
 Qy 241 PHSWNSFYRLRPELRARERKFTTMMVKDLOHHCVIHDAMSGLRHVQLRAOEFGQ 300
 Db 241 PHSWNSFYRLRPELRARERKFTTMMVKDLOHHCVIHDAMSGLRHVQLRAOEFGQ 300
 Qy 301 GEMSEWSPAMGTPMTESRSPPAENEVSTPMQALTTNKDDNLLFRDSANATSLPVEFMP 360
 Db 301 GEMSEWSPAMGTPMTESRSPPAENEVSTPMQALTTNKDDNLLFRDSANATSLPVEFMP 360
 Qy 361 VPEGDSKDVAAAP 373
 Db 357 ----ODSSSVPLP 365

RESULT 6

US-09-313-942-15
 ; Sequence 15, Application US/09313942
 ; Publication No. US20020012962A1
 ; GENERAL INFORMATION:
 ; APPLICANT: REGENERON PHARMACEUTICALS, INC.
 ; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
 ; FILE REFERENCE: REG 203-A
 ; CURRENT APPLICATION NUMBER: US/09/313,942
 ; CURRENT FILING DATE: 1999-05-19

;; PRIOR APPLICATION NUMBER: 09/313,942
;; PRIOR FILING DATE: 1999-05-19
;; PRIOR APPLICATION NUMBER: 60/101,858
;; PRIOR FILING DATE: 1998-09-25
;; NUMBER OF SEQ ID NOS: 32
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 15
;; LENGTH: 360
;; TYPE: PR1
;; ORGANISM: Homo sapiens
US-09-313-942-15

Query Match 66.8%; Score 1910; DB 9; Length 360;
Best Local Similarity 99.4%; Pred. No. 1,3e-139;
Matches 355; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLAVGCLLAAALPAAGALAPRRCPAEOVARGVLTSLPDSVTLTCPGVEPEDNATVHW 60
DB 1 MVAAGCALAALAAAPGALAPRRCPAEOVARGVLTSLPDSVTLTCPGVEPEDNATVHW 60
QY 61 VLKRPAGSHPSRWAGGRLLRSVOLHDSGNVSCYRAGRPAQTVHLVDVPEEPQLS 120
DB 61 VLKRPAGSHPSRWAGGRLLRSVOLHDSGNVSCYRAGRPAQTVHLVDVPEEPQLS 120
QY 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLVKRFQNSPAEDFOEPCQYSQESQKSCQLAV 180
DB 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLVKRFQNSPAEDFOEPCQYSQESQKSCQLAV 180
QY 181 PEGDSSFYIVSMCVASSVGSKFSKTQTFQCGGILQDPDPANITVAVARNPRMLSVTMO 240
DB 181 PEGDSSFYIVSMCVASSVGSKFSKTQTFQCGGILQDPDPANITVAVARNPRMLSVTMO 240
QY 241 PHSWNSFYRLRFEFLRYAERSKFTTMMVKDLOHCVIHDAWSGLRHVVQLRAQEEFGQ 300
DB 241 PHSWNSFYRLRFEFLRYAERSKFTTMMVKDLOHCVIHDAWSGLRHVVQLRAQEEFGQ 300
QY 301 GEMSEMSPEAMGTPTWTSRSPPAENEVSTPMQALTTNKDDNIIIFRDSANATSLPVE 357
DB 301 GEMSEMSPEAMGTPTWTSRSPPAENEVSTPMQALTTNKDDNIIIFRDSANATSLPVE 357

RESULT 7
US-09-935-868-15
; Sequence 15, Application US/09935868
; Patent No. US20020164690A1
; GENERAL INFORMATION:
; APPLICANT: Regeneron Pharmaceuticals, Inc
; TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using
; FILE REFERENCE: REG 203D
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: US/09/935,868
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 360
; TYPE: PR1
; ORGANISM: Homo sapiens
US-09-935-868-15

Query Match 66.8%; Score 1910; DB 9; Length 360;
Best Local Similarity 99.4%; Pred. No. 1,3e-139;
Matches 355; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLAVGCLLAAALPAAGALAPRRCPAEOVARGVLTSLPDSVTLTCPGVEPEDNATVHW 60
DB 1 MVAAGCALAALAAAPGALAPRRCPAEOVARGVLTSLPDSVTLTCPGVEPEDNATVHW 60
QY 61 VLKRPAGSHPSRWAGGRLLRSVOLHDSGNVSCYRAGRPAQTVHLVDVPEEPQLS 120
DB 61 VLKRPAGSHPSRWAGGRLLRSVOLHDSGNVSCYRAGRPAQTVHLVDVPEEPQLS 120

QY 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLVKRFQNSPAEDFOEPCQYSQESQKSCQLAV 180
DB 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLVKRFQNSPAEDFOEPCQYSQESQKSCQLAV 180
QY 181 PEGDSSFYIVSMCVASSVGSKFSKTQTFQCGGILQDPDPANITVAVARNPRMLSVTMO 240
DB 181 PEGDSSFYIVSMCVASSVGSKFSKTQTFQCGGILQDPDPANITVAVARNPRMLSVTMO 240
QY 241 PHSWNSFYRLRFEFLRYAERSKFTTMMVKDLOHCVIHDAWSGLRHVVQLRAQEEFGQ 300
DB 241 PHSWNSFYRLRFEFLRYAERSKFTTMMVKDLOHCVIHDAWSGLRHVVQLRAQEEFGQ 300
QY 301 GEMSEMSPEAMGTPTWTSRSPPAENEVSTPMQALTTNKDDNIIIFRDSANATSLPVE 357
DB 301 GEMSEMSPEAMGTPTWTSRSPPAENEVSTPMQALTTNKDDNIIIFRDSANATSLPVE 357

RESULT 8
US-10-287-035-15
; Sequence 15, Application US/10287035
; Publication No. US20030104567A1
; GENERAL INFORMATION:
; APPLICANT: Neil Stahl and George D. Yancopoulos
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203DA
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: USN 09/935,868
; PRIOR FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: USSN 09/787,835
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: USSN 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR FILING DATE: 1999-05-19
; PRIOR FILING DATE: 1999-05-19
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 360
; TYPE: PR1
; ORGANISM: Homo sapiens
US-10-287-035-15

Query Match 66.8%; Score 1910; DB 14; Length 360;
Best Local Similarity 99.4%; Pred. No. 1,3e-139;
Matches 355; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLAVGCLLAAALPAAGALAPRRCPAEOVARGVLTSLPDSVTLTCPGVEPEDNATVHW 60
DB 1 MVAAGCALAALAAAPGALAPRRCPAEOVARGVLTSLPDSVTLTCPGVEPEDNATVHW 60
QY 61 VLKRPAGSHPSRWAGGRLLRSVOLHDSGNVSCYRAGRPAQTVHLVDVPEEPQLS 120
DB 61 VLKRPAGSHPSRWAGGRLLRSVOLHDSGNVSCYRAGRPAQTVHLVDVPEEPQLS 120
QY 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLVKRFQNSPAEDFOEPCQYSQESQKSCQLAV 180
DB 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLVKRFQNSPAEDFOEPCQYSQESQKSCQLAV 180
QY 181 PEGDSSFYIVSMCVASSVGSKFSKTQTFQCGGILQDPDPANITVAVARNPRMLSVTMO 240
DB 181 PEGDSSFYIVSMCVASSVGSKFSKTQTFQCGGILQDPDPANITVAVARNPRMLSVTMO 240
QY 241 PHSWNSFYRLRFEFLRYAERSKFTTMMVKDLOHCVIHDAWSGLRHVVQLRAQEEFGQ 300
DB 241 PHSWNSFYRLRFEFLRYAERSKFTTMMVKDLOHCVIHDAWSGLRHVVQLRAQEEFGQ 300
QY 301 GEMSEMSPEAMGTPTWTSRSPPAENEVSTPMQALTTNKDDNIIIFRDSANATSLPVE 357
DB 301 GEMSEMSPEAMGTPTWTSRSPPAENEVSTPMQALTTNKDDNIIIFRDSANATSLPVE 357


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RESULT 9
US-10-282-162-15
; Sequence 15, Application US/10282162
; Publication No. US20030143697A1
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/10/282,162
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-282-162-15

Query Match      66.8%; Score 1910; DB 14; Length 360;
Best Local Similarity 99.4%; Pred. No. 1,36-139;
Matches 355; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAVGCALIAALLAAGALAPRRCPAEOVARGVLTSLPGDSVTLTCPGVEPEDNATVHW 60
   :|||||
Db 1 MAAVGCALIAALLAAGALAPRRCPAEOVARGVLTSLPGDSVTLTCPGVEPEDNATVHW 60

QY 61 VARKPAAGSHPSRWAMGRRLLRSVQLHDSGNVSCYRAGRPAAGTVHLLVDVPEEPOL 120
   :|||||
Db 61 VARKPAAGSHPSRWAMGRRLLRSVQLHDSGNVSCYRAGRPAAGTVHLLVDVPEEPOL 120

QY 61 VARKPAAGSHPSRWAMGRRLLRSVQLHDSGNVSCYRAGRPAAGTVHLLVDVPEEPOL 120
   :|||||
Db 61 VARKPAAGSHPSRWAMGRRLLRSVQLHDSGNVSCYRAGRPAAGTVHLLVDVPEEPOL 120

QY 121 CRRKSPLSNVVCEWGRSTPSTLTAKVILVRKFQNSPADFOEPCOYSDSOQSFSCQLAV 180
   :|||||
Db 121 CRRKSPLSNVVCEWGRSTPSTLTAKVILVRKFQNSPADFOEPCOYSDSOQSFSCQLAV 180

QY 121 CRRKSPLSNVVCEWGRSTPSTLTAKVILVRKFQNSPADFOEPCOYSDSOQSFSCQLAV 180
   :|||||
Db 121 CRRKSPLSNVVCEWGRSTPSTLTAKVILVRKFQNSPADFOEPCOYSDSOQSFSCQLAV 180

QY 181 PEGDSSFYIVSMCVASVSGSKFKSTQTFQCGILQDPDPANITVTVAARNPRLSTYWD 240
   :|||||
Db 181 PEGDSSFYIVSMCVASVSGSKFKSTQTFQCGILQDPDPANITVTVAARNPRLSTYWD 240

QY 181 PEGDSSFYIVSMCVASVSGSKFKSTQTFQCGILQDPDPANITVTVAARNPRLSTYWD 240
   :|||||
Db 181 PEGDSSFYIVSMCVASVSGSKFKSTQTFQCGILQDPDPANITVTVAARNPRLSTYWD 240

QY 241 PHSWNSFYRLRPELRRAERSKFTTMMVKDLOHHCVIDAMSGLRHVQLRAOEFPQ 300
   :|||||
Db 241 PHSWNSFYRLRPELRRAERSKFTTMMVKDLOHHCVIDAMSGLRHVQLRAOEFPQ 300

QY 241 PHSWNSFYRLRPELRRAERSKFTTMMVKDLOHHCVIDAMSGLRHVQLRAOEFPQ 300
   :|||||
Db 241 PHSWNSFYRLRPELRRAERSKFTTMMVKDLOHHCVIDAMSGLRHVQLRAOEFPQ 300

QY 301 GEWSWSPAMGTPMTESRSPPAENEVSTPMQALTTNKDDNILFRDSANATSLPV 357
   :|||||
Db 301 GEWSWSPAMGTPMTESRSPPAENEVSTPMQALTTNKDDNILFRDSANATSLPV 357

RESULT 10
US-10-322-696-144
; Sequence 144, Application US/10322696
; Publication No. US20040166490A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Malandro, Marc
; TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
; FILE REFERENCE: 529452001200
; CURRENT APPLICATION NUMBER: US/10/322,696
; CURRENT FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 144
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-322-696-144

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Query Match      63.7%; Score 1823.5; DB 16; Length 453;
Best Local Similarity 92.5%; Pred. No. 9,46-133;
Matches 345; Conservative 1; Mismatches 4; Indels 23; Gaps 2;

QY 1 MAAVGCALIAALLAAGALAPRRCPAEOVARGVLTSLPGDSVTLTCPGVEPEDNATVHW 60
   :|||||
Db 1 MAAVGCALIAALLAAGALAPRRCPAEOVARGVLTSLPGDSVTLTCPGVEPEDNATVHW 60

QY 61 VARKPAAGSHPSRWAMGRRLLRSVQLHDSGNVSCYRAGRPAAGTVHLLVDVPEEPOL 120
   :|||||
Db 61 VARKPAAGSHPSRWAMGRRLLRSVQLHDSGNVSCYRAGRPAAGTVHLLVDVPEEPOL 120

QY 61 VARKPAAGSHPSRWAMGRRLLRSVQLHDSGNVSCYRAGRPAAGTVHLLVDVPEEPOL 120
   :|||||
Db 61 VARKPAAGSHPSRWAMGRRLLRSVQLHDSGNVSCYRAGRPAAGTVHLLVDVPEEPOL 120

QY 121 CRRKSPLSNVVCEWGRSTPSTLTAKVILVRKFQNSPADFOEPCOYSDSOQSFSCQLAV 180
   :|||||
Db 121 CRRKSPLSNVVCEWGRSTPSTLTAKVILVRKFQNSPADFOEPCOYSDSOQSFSCQLAV 180

QY 121 CRRKSPLSNVVCEWGRSTPSTLTAKVILVRKFQNSPADFOEPCOYSDSOQSFSCQLAV 180
   :|||||
Db 121 CRRKSPLSNVVCEWGRSTPSTLTAKVILVRKFQNSPADFOEPCOYSDSOQSFSCQLAV 180

QY 181 PEGDSSFYIVSMCVASVSGSKFKSTQTFQCGILQDPDPANITVTVAARNPRLSTYWD 240
   :|||||
Db 181 PEGDSSFYIVSMCVASVSGSKFKSTQTFQCGILQDPDPANITVTVAARNPRLSTYWD 240

QY 181 PEGDSSFYIVSMCVASVSGSKFKSTQTFQCGILQDPDPANITVTVAARNPRLSTYWD 240
   :|||||
Db 181 PEGDSSFYIVSMCVASVSGSKFKSTQTFQCGILQDPDPANITVTVAARNPRLSTYWD 240

QY 241 PHSWNSFYRLRPELRRAERSKFTTMMVKDLOHHCVIDAMSGLRHVQLRAOEFPQ 300
   :|||||
Db 241 PHSWNSFYRLRPELRRAERSKFTTMMVKDLOHHCVIDAMSGLRHVQLRAOEFPQ 300

QY 241 PHSWNSFYRLRPELRRAERSKFTTMMVKDLOHHCVIDAMSGLRHVQLRAOEFPQ 300
   :|||||
Db 241 PHSWNSFYRLRPELRRAERSKFTTMMVKDLOHHCVIDAMSGLRHVQLRAOEFPQ 300

QY 301 GEWSWSPAMGTPMTESRSPPAENEVSTPMQALTTNKDDNILFRDSANATSLPV 360
   :|||||
Db 301 GEWSWSPAMGTPMTESRSPPAENEVSTPMQALTTNKDDNILFRDSANATSLPV 360

QY 361 VPPGDSKVVAAP 373
   :|||
Db 342 ----QDSSVPLP 350

RESULT 11
US-09-313-942-26
; Sequence 26, Application US/09313942
; Publication No. US20020012962A1
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-A
; CURRENT APPLICATION NUMBER: US/09/313,942
; CURRENT FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 1158
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-313-942-26

Query Match      62.5%; Score 1788; DB 9; Length 1158;
Best Local Similarity 99.1%; Pred. No. 26-129;
Matches 331; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAAVGCALIAALLAAGALAPRRCPAEOVARGVLTSLPGDSVTLTCPGVEPEDNATVHW 60
   :|||||
Db 1 MAAVGCALIAALLAAGALAPRRCPAEOVARGVLTSLPGDSVTLTCPGVEPEDNATVHW 60

QY 61 VARKPAAGSHPSRWAMGRRLLRSVQLHDSGNVSCYRAGRPAAGTVHLLVDVPEEPOL 120
   :|||||
Db 61 VARKPAAGSHPSRWAMGRRLLRSVQLHDSGNVSCYRAGRPAAGTVHLLVDVPEEPOL 120

QY 61 VARKPAAGSHPSRWAMGRRLLRSVQLHDSGNVSCYRAGRPAAGTVHLLVDVPEEPOL 120
   :|||||
Db 61 VARKPAAGSHPSRWAMGRRLLRSVQLHDSGNVSCYRAGRPAAGTVHLLVDVPEEPOL 120

QY 121 CRRKSPLSNVVCEWGRSTPSTLTAKVILVRKFQNSPADFOEPCOYSDSOQSFSCQLAV 180
   :|||||
Db 121 CRRKSPLSNVVCEWGRSTPSTLTAKVILVRKFQNSPADFOEPCOYSDSOQSFSCQLAV 180

QY 121 CRRKSPLSNVVCEWGRSTPSTLTAKVILVRKFQNSPADFOEPCOYSDSOQSFSCQLAV 180
   :|||||
Db 121 CRRKSPLSNVVCEWGRSTPSTLTAKVILVRKFQNSPADFOEPCOYSDSOQSFSCQLAV 180

QY 181 PEGDSSFYIVSMCVASVSGSKFKSTQTFQCGILQDPDPANITVTVAARNPRLSTYWD 240
   :|||||
Db 181 PEGDSSFYIVSMCVASVSGSKFKSTQTFQCGILQDPDPANITVTVAARNPRLSTYWD 240

```


PRIOR FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 60
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 24
LENGTH: 1168
TYPE: PRT
ORGANISM: Homo sapiens
US-10-287-035-24

Query Match 62.3%; Score 1783; DB 14; Length 1168;
Best Local Similarity 99.7%; Pred. No. 4.9e-129;
Matches 330; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLAVGALLAALAAAPGALAPRCPCPAQEVAVAGVLTSLPGDSVTLTCGVEPEDNATVHM 60
1 MVAAGCALLAALAAAPGALAPRCPCPAQEVAVAGVLTSLPGDSVTLTCGVEPEDNATVHM 60
DB 1 VLKRPAGSHPSRWAGMGRLLRLRSVOLHDSGNVSCYRAGRPAQTVHLLVDVPEEPOLLS 120
61 VLKRPAGSHPSRWAGMGRLLRLRSVOLHDSGNVSCYRAGRPAQTVHLLVDVPEEPOLLS 120
QY 121 CFRKSPLSNVVCEWGPSTPSLTITKAVLLVRKFQNSPAEDFOEQYQSQKFSQCLAV 180
61 VLKRPAGSHPSRWAGMGRLLRLRSVOLHDSGNVSCYRAGRPAQTVHLLVDVPEEPOLLS 120
DB 121 CFRKSPLSNVVCEWGPSTPSLTITKAVLLVRKFQNSPAEDFOEQYQSQKFSQCLAV 180
121 CFRKSPLSNVVCEWGPSTPSLTITKAVLLVRKFQNSPAEDFOEQYQSQKFSQCLAV 180
QY 181 PEGDSSFYIVSMCVASSVGSKFSKTQTFQCGIILQDPPANITVTAANRPMLSVTWOD 240
181 PEGDSSFYIVSMCVASSVGSKFSKTQTFQCGIILQDPPANITVTAANRPMLSVTWOD 240
DB 181 PEGDSSFYIVSMCVASSVGSKFSKTQTFQCGIILQDPPANITVTAANRPMLSVTWOD 240
181 PEGDSSFYIVSMCVASSVGSKFSKTQTFQCGIILQDPPANITVTAANRPMLSVTWOD 240
QY 241 PHSWNSFFYRLRFLRYRAERSKFTTMMVKDLOHHCVIHDAMSGLRHVQLRAQEEFGQ 300
241 PHSWNSFFYRLRFLRYRAERSKFTTMMVKDLOHHCVIHDAMSGLRHVQLRAQEEFGQ 300
DB 241 PHSWNSFFYRLRFLRYRAERSKFTTMMVKDLOHHCVIHDAMSGLRHVQLRAQEEFGQ 300
241 PHSWNSFFYRLRFLRYRAERSKFTTMMVKDLOHHCVIHDAMSGLRHVQLRAQEEFGQ 300
QY 301 GEMSEMSPEAMGTPTESRSPPAENEVSTPM 331
301 GEMSEMSPEAMGTPTESRSPPAENEVSTPM 331
DB 301 GEMSEMSPEAMGTPTESRSPPAENEVSTPM 331
301 GEMSEMSPEAMGTPTESRSPPAENEVSTPM 331

RESULT 18

US-10-282-162-24
Sequence 24, Application US/10282162
Publication No. US20030143697A1
GENERAL INFORMATION:
APPLICANT: REGENERON PHARMACEUTICALS, INC.
TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
FILE REFERENCE: REG 203-B-US
CURRENT FILING DATE: 2002-10-28
CURRENT APPLICATION NUMBER: US/10/282,162
PRIOR FILING DATE: 1999-09-22
PRIOR APPLICATION NUMBER: PCT/US99/22045
NUMBER OF SEQ ID NOS: 56
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 24
LENGTH: 1168
TYPE: PRT
ORGANISM: Homo sapiens
US-10-282-162-24

Query Match 62.3%; Score 1783; DB 14; Length 1168;
Best Local Similarity 99.7%; Pred. No. 4.9e-129;
Matches 330; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLAVGALLAALAAAPGALAPRCPCPAQEVAVAGVLTSLPGDSVTLTCGVEPEDNATVHM 60
1 MVAAGCALLAALAAAPGALAPRCPCPAQEVAVAGVLTSLPGDSVTLTCGVEPEDNATVHM 60
DB 1 VLKRPAGSHPSRWAGMGRLLRLRSVOLHDSGNVSCYRAGRPAQTVHLLVDVPEEPOLLS 120
61 VLKRPAGSHPSRWAGMGRLLRLRSVOLHDSGNVSCYRAGRPAQTVHLLVDVPEEPOLLS 120
QY 61 VLKRPAGSHPSRWAGMGRLLRLRSVOLHDSGNVSCYRAGRPAQTVHLLVDVPEEPOLLS 120
61 VLKRPAGSHPSRWAGMGRLLRLRSVOLHDSGNVSCYRAGRPAQTVHLLVDVPEEPOLLS 120
DB 61 VLKRPAGSHPSRWAGMGRLLRLRSVOLHDSGNVSCYRAGRPAQTVHLLVDVPEEPOLLS 120
61 VLKRPAGSHPSRWAGMGRLLRLRSVOLHDSGNVSCYRAGRPAQTVHLLVDVPEEPOLLS 120

QY 121 CFRKSPLSNVVCEWGPSTPSLTITKAVLLVRKFQNSPAEDFOEQYQSQKFSQCLAV 180
121 CFRKSPLSNVVCEWGPSTPSLTITKAVLLVRKFQNSPAEDFOEQYQSQKFSQCLAV 180
DB 181 PEGDSSFYIVSMCVASSVGSKFSKTQTFQCGIILQDPPANITVTAANRPMLSVTWOD 240
181 PEGDSSFYIVSMCVASSVGSKFSKTQTFQCGIILQDPPANITVTAANRPMLSVTWOD 240
DB 181 PEGDSSFYIVSMCVASSVGSKFSKTQTFQCGIILQDPPANITVTAANRPMLSVTWOD 240
181 PEGDSSFYIVSMCVASSVGSKFSKTQTFQCGIILQDPPANITVTAANRPMLSVTWOD 240
QY 241 PHSWNSFFYRLRFLRYRAERSKFTTMMVKDLOHHCVIHDAMSGLRHVQLRAQEEFGQ 300
241 PHSWNSFFYRLRFLRYRAERSKFTTMMVKDLOHHCVIHDAMSGLRHVQLRAQEEFGQ 300
DB 241 PHSWNSFFYRLRFLRYRAERSKFTTMMVKDLOHHCVIHDAMSGLRHVQLRAQEEFGQ 300
241 PHSWNSFFYRLRFLRYRAERSKFTTMMVKDLOHHCVIHDAMSGLRHVQLRAQEEFGQ 300
QY 301 GEMSEMSPEAMGTPTESRSPPAENEVSTPM 331
301 GEMSEMSPEAMGTPTESRSPPAENEVSTPM 331
DB 301 GEMSEMSPEAMGTPTESRSPPAENEVSTPM 331
301 GEMSEMSPEAMGTPTESRSPPAENEVSTPM 331

RESULT 19

US-09-313-942-16
Sequence 16, Application US/09313942
Publication No. US20020012962A1
GENERAL INFORMATION:
APPLICANT: REGENERON PHARMACEUTICALS, INC.
TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
FILE REFERENCE: REG 203-A
CURRENT FILING DATE: 1999-05-19
CURRENT APPLICATION NUMBER: US/09/313,942
PRIOR FILING DATE: 1998-09-25
PRIOR APPLICATION NUMBER: 60/101,856
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 16
LENGTH: 315
TYPE: PRT
ORGANISM: Homo sapiens
US-09-313-942-16

Query Match 58.8%; Score 1683; DB 9; Length 315;
Best Local Similarity 99.7%; Pred. No. 4.5e-122;
Matches 312; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLAVGALLAALAAAPGALAPRCPCPAQEVAVAGVLTSLPGDSVTLTCGVEPEDNATVHM 60
1 MVAAGCALLAALAAAPGALAPRCPCPAQEVAVAGVLTSLPGDSVTLTCGVEPEDNATVHM 60
DB 1 VLKRPAGSHPSRWAGMGRLLRLRSVOLHDSGNVSCYRAGRPAQTVHLLVDVPEEPOLLS 120
61 VLKRPAGSHPSRWAGMGRLLRLRSVOLHDSGNVSCYRAGRPAQTVHLLVDVPEEPOLLS 120
QY 61 VLKRPAGSHPSRWAGMGRLLRLRSVOLHDSGNVSCYRAGRPAQTVHLLVDVPEEPOLLS 120
61 VLKRPAGSHPSRWAGMGRLLRLRSVOLHDSGNVSCYRAGRPAQTVHLLVDVPEEPOLLS 120
DB 61 VLKRPAGSHPSRWAGMGRLLRLRSVOLHDSGNVSCYRAGRPAQTVHLLVDVPEEPOLLS 120
61 VLKRPAGSHPSRWAGMGRLLRLRSVOLHDSGNVSCYRAGRPAQTVHLLVDVPEEPOLLS 120
QY 121 CFRKSPLSNVVCEWGPSTPSLTITKAVLLVRKFQNSPAEDFOEQYQSQKFSQCLAV 180
121 CFRKSPLSNVVCEWGPSTPSLTITKAVLLVRKFQNSPAEDFOEQYQSQKFSQCLAV 180
DB 121 CFRKSPLSNVVCEWGPSTPSLTITKAVLLVRKFQNSPAEDFOEQYQSQKFSQCLAV 180
121 CFRKSPLSNVVCEWGPSTPSLTITKAVLLVRKFQNSPAEDFOEQYQSQKFSQCLAV 180
QY 181 PEGDSSFYIVSMCVASSVGSKFSKTQTFQCGIILQDPPANITVTAANRPMLSVTWOD 240
181 PEGDSSFYIVSMCVASSVGSKFSKTQTFQCGIILQDPPANITVTAANRPMLSVTWOD 240
DB 181 PEGDSSFYIVSMCVASSVGSKFSKTQTFQCGIILQDPPANITVTAANRPMLSVTWOD 240
181 PEGDSSFYIVSMCVASSVGSKFSKTQTFQCGIILQDPPANITVTAANRPMLSVTWOD 240
QY 241 PHSWNSFFYRLRFLRYRAERSKFTTMMVKDLOHHCVIHDAMSGLRHVQLRAQEEFGQ 300
241 PHSWNSFFYRLRFLRYRAERSKFTTMMVKDLOHHCVIHDAMSGLRHVQLRAQEEFGQ 300
DB 241 PHSWNSFFYRLRFLRYRAERSKFTTMMVKDLOHHCVIHDAMSGLRHVQLRAQEEFGQ 300
241 PHSWNSFFYRLRFLRYRAERSKFTTMMVKDLOHHCVIHDAMSGLRHVQLRAQEEFGQ 300
QY 301 GEMSEMSPEAMGTPTESRSPPAENEVSTPM 331
301 GEMSEMSPEAMGTPTESRSPPAENEVSTPM 331
DB 301 GEMSEMSPEAMGTPTESRSPPAENEVSTPM 331
301 GEMSEMSPEAMGTPTESRSPPAENEVSTPM 331

RESULT 20

US-09-935-868-16
Sequence 16, Application US/09935868
Patent No. US20020164690A1

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; GENERAL INFORMATION:
; APPLICANT: Regeneron Pharmaceuticals, Inc.
; TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using
; FILE REFERENCE: REG 203D
; CURRENT APPLICATION NUMBER: US/09/935,868
; PRIOR FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
; LENGTH: 315
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-935-868-16

Query Match      58.8%; Score 1683; DB 9; Length 315;
Best Local Similarity 99.7%; Pred. No. 4.5e-122;
Matches 312; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVAVGALLAALAAAGALAPRRCPADEVARGVLTSLPGDSVTLTCCPVEPEDNATVHM 60
DB 1 MVAVGALLAALAAAGALAPRRCPADEVARGVLTSLPGDSVTLTCCPVEPEDNATVHM 60
QY 61 VLRKPAAGSHPSRMAGMGRLLRLRSVQLHDSGNYSCYRAGRPAQVTHLLVDVPEEPOLS 120
DB 61 VLRKPAAGSHPSRMAGMGRLLRLRSVQLHDSGNYSCYRAGRPAQVTHLLVDVPEEPOLS 120
QY 121 CERKSPLSNVVCEWGRSTPSLTITKAVLLVRKFONS PADPFOBPCCYSGESQKFSQCLAV 180
DB 121 CERKSPLSNVVCEWGRSTPSLTITKAVLLVRKFONS PADPFOBPCCYSGESQKFSQCLAV 180
QY 181 PGDSSFFYIVSMCVASVSGSKFSKTQTFQCGGILQDPDPANITVTAVANPRMLSTVWOD 240
DB 181 PGDSSFFYIVSMCVASVSGSKFSKTQTFQCGGILQDPDPANITVTAVANPRMLSTVWOD 240
QY 241 PHSWNSFFYRLRPELRYRERSKFTFTVMVKDLOHHCIVHDAMSGLRHVYQLRAOBEFQ 300
DB 241 PHSWNSFFYRLRPELRYRERSKFTFTVMVKDLOHHCIVHDAMSGLRHVYQLRAOBEFQ 300
QY 301 GEMSEWSPAMGT 313
DB 301 GEMSEWSPAMGT 313

RESULT 21
US-10-287-035-16
; Sequence 16, Application US/10287035
; Publication No. US20030104567A1
; GENERAL INFORMATION:
; APPLICANT: Neil Stahl and George D. Yancopoulos
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203DA
; CURRENT APPLICATION NUMBER: US/10/287,035
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: USSN 09/935,868
; PRIOR FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: USSN 09/787,835
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: USSN 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR FILING DATE: 1999-05-19
; PRIOR FILING DATE: 1999-05-19
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FaastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 315
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-287-035-16

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Query Match      58.8%; Score 1683; DB 14; Length 315;
Best Local Similarity 99.7%; Pred. No. 4.5e-122;
Matches 312; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVAVGALLAALAAAGALAPRRCPADEVARGVLTSLPGDSVTLTCCPVEPEDNATVHM 60
DB 1 MVAVGALLAALAAAGALAPRRCPADEVARGVLTSLPGDSVTLTCCPVEPEDNATVHM 60
QY 61 VLRKPAAGSHPSRMAGMGRLLRLRSVQLHDSGNYSCYRAGRPAQVTHLLVDVPEEPOLS 120
DB 61 VLRKPAAGSHPSRMAGMGRLLRLRSVQLHDSGNYSCYRAGRPAQVTHLLVDVPEEPOLS 120
QY 121 CERKSPLSNVVCEWGRSTPSLTITKAVLLVRKFONS PADPFOBPCCYSGESQKFSQCLAV 180
DB 121 CERKSPLSNVVCEWGRSTPSLTITKAVLLVRKFONS PADPFOBPCCYSGESQKFSQCLAV 180
QY 181 PGDSSFFYIVSMCVASVSGSKFSKTQTFQCGGILQDPDPANITVTAVANPRMLSTVWOD 240
DB 181 PGDSSFFYIVSMCVASVSGSKFSKTQTFQCGGILQDPDPANITVTAVANPRMLSTVWOD 240
QY 241 PHSWNSFFYRLRPELRYRERSKFTFTVMVKDLOHHCIVHDAMSGLRHVYQLRAOBEFQ 300
DB 241 PHSWNSFFYRLRPELRYRERSKFTFTVMVKDLOHHCIVHDAMSGLRHVYQLRAOBEFQ 300
QY 301 GEMSEWSPAMGT 313
DB 301 GEMSEWSPAMGT 313

RESULT 22
US-10-282-162-16
; Sequence 16, Application US/10282162
; Publication No. US20030143697A1
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/10/282,162
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FaastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 315
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-282-162-16

Query Match      58.8%; Score 1683; DB 14; Length 315;
Best Local Similarity 99.7%; Pred. No. 4.5e-122;
Matches 312; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVAVGALLAALAAAGALAPRRCPADEVARGVLTSLPGDSVTLTCCPVEPEDNATVHM 60
DB 1 MVAVGALLAALAAAGALAPRRCPADEVARGVLTSLPGDSVTLTCCPVEPEDNATVHM 60
QY 61 VLRKPAAGSHPSRMAGMGRLLRLRSVQLHDSGNYSCYRAGRPAQVTHLLVDVPEEPOLS 120
DB 61 VLRKPAAGSHPSRMAGMGRLLRLRSVQLHDSGNYSCYRAGRPAQVTHLLVDVPEEPOLS 120
QY 121 CERKSPLSNVVCEWGRSTPSLTITKAVLLVRKFONS PADPFOBPCCYSGESQKFSQCLAV 180
DB 121 CERKSPLSNVVCEWGRSTPSLTITKAVLLVRKFONS PADPFOBPCCYSGESQKFSQCLAV 180
QY 181 PGDSSFFYIVSMCVASVSGSKFSKTQTFQCGGILQDPDPANITVTAVANPRMLSTVWOD 240
DB 181 PGDSSFFYIVSMCVASVSGSKFSKTQTFQCGGILQDPDPANITVTAVANPRMLSTVWOD 240
QY 241 PHSWNSFFYRLRPELRYRERSKFTFTVMVKDLOHHCIVHDAMSGLRHVYQLRAOBEFQ 300
DB 241 PHSWNSFFYRLRPELRYRERSKFTFTVMVKDLOHHCIVHDAMSGLRHVYQLRAOBEFQ 300
QY 301 GEMSEWSPAMGT 313
DB 301 GEMSEWSPAMGT 313

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QY 241 PHSMNSFYRLRELAAYRABRSKFTTMMVKDLOHHCVIDHAMSGLRHVVQLRAOEFGQ 300
 DB 241 PHSMNSFYRLRELAAYRABRSKFTTMMVKDLOHHCVIDHAMSGLRHVVQLRAOEFGQ 300
 QY 301 GEMSEWSPAMGT 313
 DB 301 GEMSEWSPAMGT 313

RESULT 23

US-10-322-696-141
 ; Sequence 141, Application US/10322696
 ; Publication No. US20040166490A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Morris, David W.
 ; APPLICANT: Malandro, Marc
 ; TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
 ; FILE REFERENCE: 529452001200
 ; CURRENT APPLICATION NUMBER: US/10/322,696
 ; CURRENT FILING DATE: 2003-10-17
 ; NUMBER OF SEQ ID NOS: 186
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 141
 ; LENGTH: 387
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-10-322-696-141

Query Match 33.4%; Score 954.5; DB 16; Length 387;
 Best Local Similarity 50.1%; Pred. No. 2e-65;
 Matches 188; Conservative 52; Mismatches 122; Indels 13; Gaps 5;

QY 1 MLAVGCALLAALLAAPGALAPRCPAQEVARGVLSLPGDSVTLTCGVEPEDNATVHW 60
 DB 2 MLTVGCTLLVALLAAPVALVIGSCRALEVANGVTSLPGATVTLICPKKAAGNVITHW 61
 QY 61 VLRKAAGSHPSRMAGMGRILLRSVOLHDSGNSCYRAGRPACTVHLVDVPEEPQLS 120
 DB 62 VY----SSQNRKWTGTLVLRDVLSDTDYLCSLNDHLVGTVPVLLVDVPEEPQLS 117
 QY 121 CERKSPLSNVCEWGPSTPSLTTKAVLVLRKFNSPA--DFEPCQYQSQSKSCOLA 179
 DB 118 CERKPNLVNALCEWRSSTPSTTKAVLPAKKINTNGKSDPOVPCQYQSQSKSCOVE 177
 QY 180 VPEGDSFTYVMCAVSSVGSKFSTQTOGCGILQPPRANITVTAVARNPMLSVTWQ 239
 DB 178 ILGDKVYHIVSLCVANSVGSKSHNEAFHSLKMOVQPPRANLVVSAIGRRMLKVMQ 237
 QY 240 DPHSMNSFYRLRELAAYRABRSKFTTMMVKDLOHHCVIDHAMSGLRHVVQLRAOEFG 299
 DB 238 HPETWDSYLLQPOLRYRPMVSKFTVLLPVAQYQCVIHDLRGVKNVQVRKEELD 297
 QY 300 QGEMSEWSPAMGTPTW--TESRSPPAENEVSTPMQALTTKKDDNILFRDSANATSLPYEF 358
 DB 298 LGQSEWSPBVTGTPWIAEPRTTPA--GILMNPQVSDSANHDEQYSSSTATSV---- 352
 QY 359 MPVPGEDSKDVAP 373
 DB 353 --LAPVOESSMSLIP 365

RESULT 24

US-10-247-463-13
 ; Sequence 13, Application US/10247463
 ; Publication No. US20030082734A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dowling, Lynette M.
 ; APPLICANT: Timans, Jacqueline C.
 ; APPLICANT: Gorman, Daniel M.
 ; APPLICANT: Kastellein, Robert A.
 ; APPLICANT: Bazar, J. Fernando
 ; TITLE OF INVENTION: Mammalian Receptor Proteins; Related Reagents and
 ; TITLE OF INVENTION: Methods

FILE REFERENCE: DX09920
 ; CURRENT APPLICATION NUMBER: US/10/247,463
 ; CURRENT FILING DATE: 2002-09-18
 ; PRIOR APPLICATION NUMBER: US/09/598,113
 ; PRIOR FILING DATE: 2000-05-31
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 13
 ; LENGTH: 460
 ; TYPE: PRT
 ; ORGANISM: rodent
 US-10-247-463-13

Query Match 33.4%; Score 954.5; DB 14; Length 460;
 Best Local Similarity 50.1%; Pred. No. 2.6e-65;
 Matches 188; Conservative 52; Mismatches 122; Indels 13; Gaps 5;

QY 1 MLAVGCALLAALLAAPGALAPRCPAQEVARGVLSLPGDSVTLTCGVEPEDNATVHW 60
 DB 1 MLTVGCTLLVALLAAPVALVIGSCRALEVANGVTSLPGATVTLICPKKAAGNVITHW 60
 QY 61 VLRKAAGSHPSRMAGMGRILLRSVOLHDSGNSCYRAGRPACTVHLVDVPEEPQLS 120
 DB 61 VY----SSQNRKWTGTLVLRDVLSDTDYLCSLNDHLVGTVPVLLVDVPEEPQLS 116
 QY 121 CERKSPLSNVCEWGPSTPSLTTKAVLVLRKFNSPA--DFEPCQYQSQSKSCOLA 179
 DB 117 CERKPNLVNALCEWRSSTPSTTKAVLPAKKINTNGKSDPOVPCQYQSQSKSCOVE 176
 QY 180 VPEGDSFTYVMCAVSSVGSKFSTQTOGCGILQPPRANITVTAVARNPMLSVTWQ 239
 DB 177 ILGDKVYHIVSLCVANSVGSKSHNEAFHSLKMOVQPPRANLVVSAIGRRMLKVMQ 236
 QY 240 DPHSMNSFYRLRELAAYRABRSKFTTMMVKDLOHHCVIDHAMSGLRHVVQLRAOEFG 299
 DB 237 HPETWDSYLLQPOLRYRPMVSKFTVLLPVAQYQCVIHDLRGVKNVQVRKEELD 296
 QY 300 QGEMSEWSPAMGTPTW--TESRSPPAENEVSTPMQALTTKKDDNILFRDSANATSLPYEF 358
 DB 297 LGQSEWSPBVTGTPWIAEPRTTPA--GILMNPQVSDSANHDEQYSSSTATSV---- 351
 QY 359 MPVPGEDSKDVAP 373
 DB 352 --LAPVOESSMSLIP 364

RESULT 25

US-09-854-280-14
 ; Sequence 14, Application US/09854280
 ; Patent No. US20020052027A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Chen, Jian
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Gurney, Austin
 ; APPLICANT: Li, Hanzhong
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
 ; FILE REFERENCE: P1381R1C2
 ; CURRENT APPLICATION NUMBER: US/09/854,280
 ; CURRENT FILING DATE: 2001-05-10
 ; PRIOR APPLICATION NUMBER: US 09/311,832
 ; PRIOR FILING DATE: 1999-05-14
 ; PRIOR APPLICATION NUMBER: US 60/085,579
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: US 60/113,621
 ; PRIOR FILING DATE: 1998-12-23
 ; NUMBER OF SEQ ID NOS: 26
 ; SEQ ID NO 14
 ; LENGTH: 212
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-854-280-14

Query Match 32.8%; Score 938.5; DB 9; Length 212;
Best Local Similarity 97.9%; Pred. No. 1.5e-64;
Matches 187; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 354 LPVEF-MPVPGSDSDVAAPHROPLTSSERIDKQIRYILDGISAARKETCNKSNMCESS 412
DB 22 LPAAPAPVPBGSDSDVAAPHROPLTSSERIDKQIRYILDGISAARKETCNKSNMCESS 81

QY 413 KEALAENNINLPRMAEKDCGFOGFEETCLVKIITGLLEFEVYLYLQNRPFSSSEQAR 472
DB 82 KEALAENNINLPRMAEKDCGFOGFEETCLVKIITGLLEFEVYLYLQNRPFSSSEQAR 141

QY 473 AVOMSTKVLIOFLQKAKNLDATITPDPTTNASLITKLOAONQWLODMTHILRSFKER 532
DB 142 AVOMSTKVLIOFLQKAKNLDATITPDPTTNASLITKLOAONQWLODMTHILRSFKER 201

QY 533 LOSSLRALROM 543
DB 202 LOSSLRALROM 212

RESULT 26
US-09-854-208-14
; Sequence 14, Application US/09854208
; Patent No. US20020106743A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Jian
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin
; APPLICANT: Li, Hanzhong
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES
; FILE REFERENCE: P1381-R1
; CURRENT APPLICATION NUMBER: US/09/854,208
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: US/09/311,832
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/085,579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: US 60/113,621
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 26
; SEQ ID NO 14
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-208-14

Query Match 32.8%; Score 938.5; DB 9; Length 212;
Best Local Similarity 97.9%; Pred. No. 1.5e-64;
Matches 187; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 354 LPVEF-MPVPGSDSDVAAPHROPLTSSERIDKQIRYILDGISAARKETCNKSNMCESS 412
DB 22 LPAAPAPVPBGSDSDVAAPHROPLTSSERIDKQIRYILDGISAARKETCNKSNMCESS 81

QY 413 KEALAENNINLPRMAEKDCGFOGFEETCLVKIITGLLEFEVYLYLQNRPFSSSEQAR 472
DB 82 KEALAENNINLPRMAEKDCGFOGFEETCLVKIITGLLEFEVYLYLQNRPFSSSEQAR 141

QY 473 AVOMSTKVLIOFLQKAKNLDATITPDPTTNASLITKLOAONQWLODMTHILRSFKER 532
DB 142 AVOMSTKVLIOFLQKAKNLDATITPDPTTNASLITKLOAONQWLODMTHILRSFKER 201

QY 533 LOSSLRALROM 543
DB 202 LOSSLRALROM 212

RESULT 27

US-10-099-007A-3
; Sequence 3, Application US/10099007A
; Publication No. US20030017150A1
; GENERAL INFORMATION:
; APPLICANT: Theodore Torphy
; TITLE OF INVENTION: CHRONIC OBSTRUCTIVE PULMONARY DISEASE-RELATED IMMUNOGLOBULIN
; FILE REFERENCE: CEN-0286
; CURRENT APPLICATION NUMBER: US/10/099,007A
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver 2.0
; SEQ ID NO 3
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-099-007A-3

Query Match 32.8%; Score 938.5; DB 14; Length 212;
Best Local Similarity 97.9%; Pred. No. 1.5e-64;
Matches 187; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 354 LPVEF-MPVPGSDSDVAAPHROPLTSSERIDKQIRYILDGISAARKETCNKSNMCESS 412
DB 22 LPAAPAPVPBGSDSDVAAPHROPLTSSERIDKQIRYILDGISAARKETCNKSNMCESS 81

QY 413 KEALAENNINLPRMAEKDCGFOGFEETCLVKIITGLLEFEVYLYLQNRPFSSSEQAR 472
DB 82 KEALAENNINLPRMAEKDCGFOGFEETCLVKIITGLLEFEVYLYLQNRPFSSSEQAR 141

QY 473 AVOMSTKVLIOFLQKAKNLDATITPDPTTNASLITKLOAONQWLODMTHILRSFKER 532
DB 142 AVOMSTKVLIOFLQKAKNLDATITPDPTTNASLITKLOAONQWLODMTHILRSFKER 201

QY 533 LOSSLRALROM 543
DB 202 LOSSLRALROM 212

RESULT 28
US-10-400-377-13
; Sequence 13, Application US/10400377
; Publication No. US20030162949A1
; GENERAL INFORMATION:
; APPLICANT: Cox III, George N.
; APPLICANT: Bolder Biotechnology, Inc.
; TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
; FILE REFERENCE: 4152-1-PUS
; CURRENT APPLICATION NUMBER: US/10/400,377
; PRIOR FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: US/09/462,941
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/052,516
; PRIOR FILING DATE: 1997-07-14
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-400-377-13

Query Match 32.8%; Score 938.5; DB 14; Length 212;
Best Local Similarity 97.9%; Pred. No. 1.5e-64;
Matches 187; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 354 LPVEF-MPVPGSDSDVAAPHROPLTSSERIDKQIRYILDGISAARKETCNKSNMCESS 412
DB 22 LPAAPAPVPBGSDSDVAAPHROPLTSSERIDKQIRYILDGISAARKETCNKSNMCESS 81

QY 413 KEALAENNINLPRMAEKDCGFOGFEETCLVKIITGLLEFEVYLYLQNRPFSSSEQAR 472
DB 82 KEALAENNINLPRMAEKDCGFOGFEETCLVKIITGLLEFEVYLYLQNRPFSSSEQAR 141

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QY      473 AVQMSKTVLIQIOLQKAKNLDATITPPPTNASLITKLOAQONQWLODMTHLILRSFEK 532
      142 AVQMSKTVLIQIOLQKAKNLDATITPPPTNASLITKLOAQONQWLODMTHLILRSFEK 201
Db      533 LOSSLRALROM 543
      202 LOSSLRALROM 212

RESULT 29
US-10-400-708-13
; Sequence 13, Application US/10400708
; Publication No. US20030166865A1
; GENERAL INFORMATION:
; APPLICANT: Cox III, George N
; APPLICANT: Bolder Biotechnology, Inc.
; TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
; FILE REFERENCE: 4152-1-PUS
; CURRENT APPLICATION NUMBER: US/10/400,708
; CURRENT FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: US/09/462,941
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/052,516
; PRIOR FILING DATE: 1997-07-14
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 13
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-400-708-13

Query Match      32.8%; Score 938.5; DB 14; Length 212;
Best Local Similarity 97.9%; Pred. No. 1.5e-64;
Matches 187; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY      354 LPVEF-MVPPEGDSKDVAAPHROPLTSSERIDKQIRYILDGISALRKETCNKSNMCESS 412
      22 LPAAFPAPVPPGDSKDVAAPHROPLTSSERIDKQIRYILDGISALRKETCNKSNMCESS 81
Db      413 KEALAENNINLPKMAEKDGCFOGSENEETCLVKIITGLLEFEVYLYLONRFESSEBOAR 472
      82 KEALAENNINLPKMAEKDGCFOGSENEETCLVKIITGLLEFEVYLYLONRFESSEBOAR 141
QY      473 AVQMSKTVLIQIOLQKAKNLDATITPPPTNASLITKLOAQONQWLODMTHLILRSFEK 532
      142 AVQMSKTVLIQIOLQKAKNLDATITPPPTNASLITKLOAQONQWLODMTHLILRSFEK 201
Db      533 LOSSLRALROM 543
      202 LOSSLRALROM 212

RESULT 30
US-10-298-148-13
; Sequence 13, Application US/10298148
; Publication No. US20030171284A1
; GENERAL INFORMATION:
; APPLICANT: Cox III, George N
; APPLICANT: Bolder Biotechnology, Inc.
; TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
; FILE REFERENCE: 4152-1-PUS
; CURRENT APPLICATION NUMBER: US/10/298,148
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US/09/462,941
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/052,516
; PRIOR FILING DATE: 1997-07-14
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 13
; LENGTH: 212
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-298-148-13

Query Match      32.8%; Score 938.5; DB 14; Length 212;
Best Local Similarity 97.9%; Pred. No. 1.5e-64;
Matches 187; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY      354 LPVEF-MVPPEGDSKDVAAPHROPLTSSERIDKQIRYILDGISALRKETCNKSNMCESS 412
      22 LPAAFPAPVPPGDSKDVAAPHROPLTSSERIDKQIRYILDGISALRKETCNKSNMCESS 81
Db      413 KEALAENNINLPKMAEKDGCFOGSENEETCLVKIITGLLEFEVYLYLONRFESSEBOAR 472
      82 KEALAENNINLPKMAEKDGCFOGSENEETCLVKIITGLLEFEVYLYLONRFESSEBOAR 141
QY      473 AVQMSKTVLIQIOLQKAKNLDATITPPPTNASLITKLOAQONQWLODMTHLILRSFEK 532
      142 AVQMSKTVLIQIOLQKAKNLDATITPPPTNASLITKLOAQONQWLODMTHLILRSFEK 201
Db      533 LOSSLRALROM 543
      202 LOSSLRALROM 212

RESULT 31
US-10-440-464-61
; Sequence 61, Application US/10440464
; Publication No. US20040018528A1
; GENERAL INFORMATION:
; APPLICANT: DEPRIMO, SAMUEL
; APPLICANT: O'FARRELL, ANNE-MARIE
; APPLICANT: MORIMOTO, AYESA
; APPLICANT: SMOLICH, BEVERLY
; APPLICANT: MANNING, WILLIAM
; APPLICANT: WALTER, SARAH
; APPLICANT: CHERINGTON, JULIE
; APPLICANT: SCHILLING, JIM
; TITLE OF INVENTION: NOVEL BIOMARKERS OF TYROSINE KINASE INHIBITOR EXPOSURE
; FILE REFERENCE: AND ACTIVITY IN MAMMALS
; CURRENT APPLICATION NUMBER: US/10/440,464
; CURRENT FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: 60/380,872
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/448,922
; PRIOR FILING DATE: 2003-02-24
; PRIOR APPLICATION NUMBER: 60/448,874
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 185
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 61
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-440-464-61

Query Match      32.8%; Score 938.5; DB 15; Length 212;
Best Local Similarity 97.9%; Pred. No. 1.3e-64;
Matches 187; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY      354 LPVEF-MVPPEGDSKDVAAPHROPLTSSERIDKQIRYILDGISALRKETCNKSNMCESS 412
      22 LPAAFPAPVPPGDSKDVAAPHROPLTSSERIDKQIRYILDGISALRKETCNKSNMCESS 81
Db      413 KEALAENNINLPKMAEKDGCFOGSENEETCLVKIITGLLEFEVYLYLONRFESSEBOAR 472
      82 KEALAENNINLPKMAEKDGCFOGSENEETCLVKIITGLLEFEVYLYLONRFESSEBOAR 141
QY      473 AVQMSKTVLIQIOLQKAKNLDATITPPPTNASLITKLOAQONQWLODMTHLILRSFEK 532
      142 AVQMSKTVLIQIOLQKAKNLDATITPPPTNASLITKLOAQONQWLODMTHLILRSFEK 201
Db      533 LOSSLRALROM 543
      202 LOSSLRALROM 212
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QY 533 LOSSLRALROM 543
 Db 202 LOSSLRALROM 212

RESULT 32

US-10-773-939-13
 ; Sequence 13, Application US/10773939
 ; Publication No. US20040175356A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cox III, George N
 ; APPLICANT: Bolder Biotechnology, Inc.
 ; TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
 ; FILE REFERENCE: 4152-1-PUS
 ; CURRENT APPLICATION NUMBER: US/10/773,939
 ; CURRENT FILING DATE: 2004-02-05
 ; PRIOR APPLICATION NUMBER: US/10/400,377
 ; PRIOR FILING DATE: 2003-03-26
 ; PRIOR APPLICATION NUMBER: US/09/462,941
 ; PRIOR FILING DATE: 2000-01-14
 ; PRIOR APPLICATION NUMBER: 60/052,516
 ; PRIOR FILING DATE: 1997-07-14
 ; NUMBER OF SEQ ID NOS: 41
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 13
 ; LENGTH: 212
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-773-939-13

Query Match 32.8%; Score 938.5; DB 16; Length 212;
 Best Local Similarity 97.9%; Pred. No. 1.5e-64;
 Matches 187; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 354 LPVEF-MPVPGEDSKDVAAPHROPLTSSERIDKQIRYILDGISAIRKETCNKSNCESS 412
 |||||
 Db 22 LPAAPAPVPPEGDSKDVAAPHROPLTSSERIDKQIRYILDGISAIRKETCNKSNCESS 81
 |||||
 QY 413 KEALAENNINLPMAEKDCGFOGFEETCLVKIITGLLEFEVYLEYLONRPFSSSEOR 472
 |||||
 Db 82 KEALAENNINLPMAEKDCGFOGFEETCLVKIITGLLEFEVYLEYLONRPFSSSEOR 141
 |||||
 QY 473 AVQMSKVLIOFLQKAKKLDATITPDPTTNASLITKLQANQWLODMTHLILRSFKF 532
 |||||
 Db 142 AVQMSKVLIOFLQKAKKLDATITPDPTTNASLITKLQANQWLODMTHLILRSFKF 201
 |||||
 QY 533 LOSSLRALROM 543
 Db 202 LOSSLRALROM 212

RESULT 33

US-10-774-149-13
 ; Sequence 13, Application US/10774149
 ; Publication No. US20040175800A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cox III, George N
 ; APPLICANT: Bolder Biotechnology, Inc.
 ; TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
 ; FILE REFERENCE: 4152-1-PUS
 ; CURRENT APPLICATION NUMBER: US/10/774,149
 ; CURRENT FILING DATE: 2004-02-05
 ; PRIOR APPLICATION NUMBER: US/10/400,377
 ; PRIOR FILING DATE: 2003-03-26
 ; PRIOR APPLICATION NUMBER: US/09/462,941
 ; PRIOR FILING DATE: 2000-01-14
 ; PRIOR APPLICATION NUMBER: 60/052,516
 ; PRIOR FILING DATE: 1997-07-14
 ; NUMBER OF SEQ ID NOS: 41
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 13
 ; LENGTH: 212
 ; TYPE: PRT

; ORGANISM: Homo sapiens
 US-10-774-149-13

Query Match 32.8%; Score 938.5; DB 16; Length 212;
 Best Local Similarity 97.9%; Pred. No. 1.5e-64;
 Matches 187; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 354 LPVEF-MPVPGEDSKDVAAPHROPLTSSERIDKQIRYILDGISAIRKETCNKSNCESS 412
 |||||
 Db 22 LPAAPAPVPPEGDSKDVAAPHROPLTSSERIDKQIRYILDGISAIRKETCNKSNCESS 81
 |||||
 QY 413 KEALAENNINLPMAEKDCGFOGFEETCLVKIITGLLEFEVYLEYLONRPFSSSEOR 472
 |||||
 Db 82 KEALAENNINLPMAEKDCGFOGFEETCLVKIITGLLEFEVYLEYLONRPFSSSEOR 141
 |||||
 QY 473 AVQMSKVLIOFLQKAKKLDATITPDPTTNASLITKLQANQWLODMTHLILRSFKF 532
 |||||
 Db 142 AVQMSKVLIOFLQKAKKLDATITPDPTTNASLITKLQANQWLODMTHLILRSFKF 201
 |||||
 QY 533 LOSSLRALROM 543
 Db 202 LOSSLRALROM 212

RESULT 34

US-10-773-654-13
 ; Sequence 13, Application US/10773654
 ; Publication No. US20040214287A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cox III, George N
 ; APPLICANT: Bolder Biotechnology, Inc.
 ; TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
 ; FILE REFERENCE: 4152-1-PUS
 ; CURRENT APPLICATION NUMBER: US/10/773,654
 ; CURRENT FILING DATE: 2004-02-05
 ; PRIOR APPLICATION NUMBER: US/10/400,377
 ; PRIOR FILING DATE: 2003-03-26
 ; PRIOR APPLICATION NUMBER: US/09/462,941
 ; PRIOR FILING DATE: 2000-01-14
 ; PRIOR APPLICATION NUMBER: 60/052,516
 ; PRIOR FILING DATE: 1997-07-14
 ; NUMBER OF SEQ ID NOS: 41
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 13
 ; LENGTH: 212
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-773-654-13

Query Match 32.8%; Score 938.5; DB 17; Length 212;
 Best Local Similarity 97.9%; Pred. No. 1.5e-64;
 Matches 187; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 354 LPVEF-MPVPGEDSKDVAAPHROPLTSSERIDKQIRYILDGISAIRKETCNKSNCESS 412
 |||||
 Db 22 LPAAPAPVPPEGDSKDVAAPHROPLTSSERIDKQIRYILDGISAIRKETCNKSNCESS 81
 |||||
 QY 413 KEALAENNINLPMAEKDCGFOGFEETCLVKIITGLLEFEVYLEYLONRPFSSSEOR 472
 |||||
 Db 82 KEALAENNINLPMAEKDCGFOGFEETCLVKIITGLLEFEVYLEYLONRPFSSSEOR 141
 |||||
 QY 473 AVQMSKVLIOFLQKAKKLDATITPDPTTNASLITKLQANQWLODMTHLILRSFKF 532
 |||||
 Db 142 AVQMSKVLIOFLQKAKKLDATITPDPTTNASLITKLQANQWLODMTHLILRSFKF 201
 |||||
 QY 533 LOSSLRALROM 543
 Db 202 LOSSLRALROM 212

RESULT 35
 US-10-828-343-3
 ; Sequence 3, Application US/10828343

```

; Publication No. US2004022838A1
; GENERAL INFORMATION:
; APPLICANT: FLECKENSTEIN, Bernhard
; ALBRECHT, Jens-Christian
; NEIPEL, Frank
; FRIEDMAN-KIEN, Alvin
; HUANG, Yao-Qi
; TITLE OF INVENTION: VIRAL INTERLEUKIN-6
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/828,343
; FILING DATE: 21-Apr-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/230,048
; FILING DATE: 12-Mar-1999
; APPLICATION NUMBER: WO PCT/EP96/03199
; FILING DATE: 19-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Granados, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 058315/0129
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 212 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-828-343-3

Query Match      32.8%; Score 938.5; DB 17; Length 212;
Best Local Similarity 97.9%; Pred. No. 1.5e-64;
Matches 187; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 354 LPVEF-MPVPGEDSKDVAAPHROPJTSSERIDKQIRYITLDGISALRKETCNKSNMCESS 412
DB 22 LPAAPAPVPPEGDSKDVAAPHROPJTSSERIDKQIRYITLDGISALRKETCNKSNMCESS 81
QY 413 KEALAENNINLPKMAEKDGCFOGSGFNETCLVKIITGLLEFVYLEYIQNRFSSSEQAR 472
DB 82 KEALAENNINLPKMAEKDGCFOGSGFNETCLVKIITGLLEFVYLEYIQNRFSSSEQAR 141
QY 473 AVOMSTKVLIOFLQKAKNLDATITPDPTTNASLITKLOAQONQMDMTHTLILRSFKER 532
DB 142 AVOMSTKVLIOFLQKAKNLDATITPDPTTNASLITKLOAQONQMDMTHTLILRSFKER 201
QY 533 LQSSLRALROM 543
DB 202 LQSSLRALROM 212

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RESULT 36
US-10-866-540-13
; Sequence 13, Application US/10866540
; Publication No. US20040230040A1
; GENERAL INFORMATION:

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; APPLICANT: Cox III, George N
; Bolder Biotechnology, Inc.
; TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
; FILE REFERENCE: 4152-1-PUS
; CURRENT APPLICATION NUMBER: US/10/866,540
; PRIOR FILING DATE: 2004-06-10
; PRIOR APPLICATION NUMBER: US/10/400,377
; PRIOR FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: US/09/462,941
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/052,516
; PRIOR FILING DATE: 1997-07-14
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 13
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-866-540-13

```

```

Query Match      32.8%; Score 938.5; DB 17; Length 212;
Best Local Similarity 97.9%; Pred. No. 1.5e-64;
Matches 187; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 354 LPVEF-MPVPGEDSKDVAAPHROPJTSSERIDKQIRYITLDGISALRKETCNKSNMCESS 412
DB 22 LPAAPAPVPPEGDSKDVAAPHROPJTSSERIDKQIRYITLDGISALRKETCNKSNMCESS 81
QY 413 KEALAENNINLPKMAEKDGCFOGSGFNETCLVKIITGLLEFVYLEYIQNRFSSSEQAR 472
DB 82 KEALAENNINLPKMAEKDGCFOGSGFNETCLVKIITGLLEFVYLEYIQNRFSSSEQAR 141
QY 473 AVOMSTKVLIOFLQKAKNLDATITPDPTTNASLITKLOAQONQMDMTHTLILRSFKER 532
DB 142 AVOMSTKVLIOFLQKAKNLDATITPDPTTNASLITKLOAQONQMDMTHTLILRSFKER 201
QY 533 LQSSLRALROM 543
DB 202 LQSSLRALROM 212

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RESULT 37
US-10-276-642-6
; Sequence 6, Application US/10276642
; Publication No. US2004023156A1
; GENERAL INFORMATION:
; APPLICANT: Ralph, Stephen John
; TITLE OF INVENTION: IMMUNE POTENTIATING COMPOSITIONS
; FILE REFERENCE: DAVI200.001APC
; CURRENT APPLICATION NUMBER: US/10/276,642
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: PCT/AU01/00565
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: PQ 7553
; PRIOR FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-276-642-6

Query Match      32.8%; Score 938.5; DB 17; Length 212;
Best Local Similarity 97.9%; Pred. No. 1.5e-64;
Matches 187; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 354 LPVEF-MPVPGEDSKDVAAPHROPJTSSERIDKQIRYITLDGISALRKETCNKSNMCESS 412
DB 22 LPAAPAPVPPEGDSKDVAAPHROPJTSSERIDKQIRYITLDGISALRKETCNKSNMCESS 81
QY 413 KEALAENNINLPKMAEKDGCFOGSGFNETCLVKIITGLLEFVYLEYIQNRFSSSEQAR 472

```

DB 82 KEALAENNINLPMAEKDCFGSGFNEETCLVITGLLEFEVYLEYLQNRFSSSEQR 141
QY 473 AVOMSTKVLIOFQKAKNLDATTPDPTTNASLLTKLQANQWLODMTHLLRSFKRF 532
DB 142 AVOMSTKVLIOFQKAKNLDATTPDPTTNASLLTKLQANQWLODMTHLLRSFKRF 201
QY 533 LOSSLRALROM 543
DB 202 LOSSLRALROM 212

RESULT 38
US-10-763-619-8
Sequence 8, Application US/10763619
Publication No. US20040215008A1
GENERAL INFORMATION:
APPLICANT: Biochemie Gesellschaft m.b.H.
TITLE OF INVENTION: Production of proteins
FILE REFERENCE: G-31109/A/BCK
CURRENT APPLICATION NUMBER: US/10/763,619
CURRENT FILING DATE: 2004-01-23
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 347
TYPE: PRF
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: Oligo-nucleotide purification aid combined with
OTHER INFORMATION: sequences of Pestivirus and Homo sapiens
US-10-763-619-8

Query Match 32.7%; Score 936.5; DB 17; Length 347;
Best Local Similarity 94.9%; Pred. No. 4,4e-64;
Matches 187; Conservative 2; Mismatches 5; Indels 3; Gaps 1;

QY 350 NATSLPV---EFMPVPGEDSKDVAAPHROPLTSSSRIDKQIRYILDGISAARKETCNKS 406
DB 151 NPTNCDLWMTSCAPVPGEDSKDVAAPHROPLTSSSRIDKQIRYILDGISAARKETCNKS 210
QY 407 NNCESSEKALAENNINLPMAEKDCFGSGFNEETCLVITGLLEFEVYLEYLQNRFES 466
DB 211 NNCESSEKALAENNINLPMAEKDCFGSGFNEETCLVITGLLEFEVYLEYLQNRFES 270
QY 467 SEEOARAVOMSTKVLIOFQKAKNLDATTPDPTTNASLLTKLQANQWLODMTHLL 526
DB 271 SEEOARAVOMSTKVLIOFQKAKNLDATTPDPTTNASLLTKLQANQWLODMTHLL 330
QY 527 RSFKERLOSSLRALROM 543
DB 331 RSFKERLOSSLRALROM 347

RESULT 39
US-10-083-446-145
Sequence 145, Application US/10083446
Publication No. US20030185790A1
GENERAL INFORMATION:
APPLICANT: Abrams, Mark A.
Bauer, S. C.
Braford-Goldberg, Sarah R.
Caparon, Maite H.
Easton, Alan M.
Klein, Barbara K.
McKeown, John P.
Olins, Peter O.
Paik, Kumnan
Thomas, John W.
TITLE OF INVENTION: Methods Of Ex-Vivo Expansion Of Hematopoietic Cells
Using Multivariant (IL-3) Hematopoiesis Chimera Proteins
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:

ADDRESSEE: S. Christopher Bauer, Pharmacia Corporation
Corporate Patent Dept., Mail Zone 04E
STREET: 800 N. Lindbergh
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63167
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/083,446
FILING DATE: 26-Feb-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/762,227
FILING DATE: 09-DEC-1996
APPLICATION NUMBER: US 08/192,325
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: US 08/446,872
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: S. Christopher Bauer
REGISTRATION NUMBER: 42,305
REFERENCE/DOCKET NUMBER: C-2790/6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (636)737-6257
TELEFAX: (636)737-5452
INFORMATION FOR SEQ ID NO: 145:
SEQUENCE CHARACTERISTICS:
LENGTH: 317 amino acids
TYPE: amino acid
STRANDEDNESS: <unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 145:
US-10-083-446-145

Query Match 32.7%; Score 935; DB 14; Length 317;
Best Local Similarity 63.0%; Pred. No. 5e-64;
Matches 206; Conservative 17; Mismatches 48; Indels 56; Gaps 7;

QY 240 DPHSNNSFYRLRFEIRYARSKRTFTMYVDLQ-----HCVIDAMSGLR 287
DB 24 DPHNNSBMDIMERNLRTPNILAFVR-AVHLENAAGIEAILRNLQCLPEATAPSR 82
QY 288 HVYQLRAQEFQGESEWS-----PEAMGTPT-ESRSPAEVSTPMQALTT 336
DB 83 HPIITIA-----GDMQERREKLTFLVTLLEQOEQVIEGRISFGG----- 125
QY 337 NKDDNILFRDSANATSLPVEFMPVPGEDSKDVAAPHROPLTSSSRIDKQIRYILDG 396
DB 126 -----SGGGSNM-----APVPGEDSKDVAAPHROPLTSSSRIDKQIRYILDG 170
QY 397 ARKETCNKSNNCESSEKALAENNINLPMAEKDCFGSGFNEETCLVITGLLEFEVY 456
DB 171 ARKETCNKSNNCESSEKALAENNINLPMAEKDCFGSGFNEETCLVITGLLEFEVY 230
QY 457 LEYLQNRFSSSEEOARAVOMSTKVLIOFQKAKNLDATTPDPTTNASLLTKLQANQW 516
DB 231 LEYLQNRFSSSEEOARAVOMSTKVLIOFQKAKNLDATTPDPTTNASLLTKLQANQW 290
QY 517 LODMTTHLLRSFKERLOSSLRALROM 543
DB 291 LODMTTHLLRSFKERLOSSLRALROM 317

RESULT 40
US-10-053-355A-3
Sequence 3, Application US/10053355A
Publication No. US20030077824A1

Fri Dec 10 08:14:23 2004

us-09-462-416-7.rapb

GENERAL INFORMATION:
APPLICANT: Rossi, Alex
TITLE OF INVENTION: Production of Cultured Human Mast Cells and Basophils for High TH
TITLE OF INVENTION: Small Molecule Drug Discovery
FILE REFERENCE: A-70982/RMS/AMS
CURRENT APPLICATION NUMBER: US/10/053,355A
CURRENT FILING DATE: 2002-06-18
PRIOR APPLICATION NUMBER: US 60/316,723
PRIOR FILING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 42
SOFTWARE: patentin version 3.1
SEQ ID NO 3
LENGTH: 184
TYPE: PRT
ORGANISM: Homo sapiens
US-10-053-355A-3

Query Match 32.6%; Score 934; DB 14; Length 184;
Best Local Similarity 100.0%; Pred. No. 2.8e-64; Indels 0; Gaps 0;
Matches 184; Conservative 0; Mismatches 0;

QY 360 PVPFGEDSKDVAAAPHROPLTSSERIDKQIRYILDGISALRKETCNKSNMCESSKEALAE 419
DB 1 PVPFGEDSKDVAAAPHROPLTSSERIDKQIRYILDGISALRKETCNKSNMCESSKEALAE 60
QY 420 NNLPMMAEKDGCFOGFEETCLVKITITGLIEFEVYLEYONRFESSEBOARAVOMSTK 479
DB 61 NNLPMMAEKDGCFOGFEETCLVKITITGLIEFEVYLEYONRFESSEBOARAVOMSTK 120
QY 480 VLIQFOAKKXNDATITPPTTNASILTKLOANOWLODMTTHILRSFKEFIQSLRA 539
DB 121 VLIQFOAKKXNDATITPPTTNASILTKLOANOWLODMTTHILRSFKEFIQSLRA 180
QY 540 LROM 543
DB 181 LROM 184

Search completed: December 9, 2004, 09:37:51
Job time : 193.417 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 9, 2004, 08:40:41 : Search time 5.96223 Seconds
(without alignments)
1254.542 Million cell updates/sec

Title: US-09-462-416-1
Perfect score: 67
Sequence: 1 EFGAGLVGQGM 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues
Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 02: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	68.7	382	2 Q8U787	Q8U787 agrobacteri
2	46	68.7	402	2 Q7CVA1	Q7CVA1 klebsiella
3	46	68.7	1171	1 N1R1_KLEPN	P03833 klebsiella
4	42	62.7	160	2 Q7S5M3	Q7S5M3 ashyia goss
5	42	62.7	160	2 AAS53165	AAS53165 ashyia go
6	42	62.7	396	2 Q9R823	Q9R823 deinococcus
7	42	62.7	540	2 Q6CC56	Q6CC56 yarrowia li
8	41	61.2	155	2 Q92P15	Q92P15 rhizobium m
9	41	61.2	291	2 Q84633	Q84633 chlamydia t
10	41	61.2	313	1 ATRX_YEAST	Q12067 saccharomyc
11	41	61.2	313	2 AAS56363	AAS56363 saccharom
12	41	61.2	319	2 Q82N27	Q82N27 streptomyces
13	41	61.2	331	2 Q6FMS6	Q6FMS6 candida gla
14	41	61.2	347	2 Q916G8	Q916G8 pseudomonas
15	41	61.2	444	2 Q74EW6	Q74EW6 geobacter s
16	41	61.2	444	2 AAR34173	AAR34173 geobacter
17	41	61.2	623	1 YFE9_YEAST	P43544 saccharomyc
18	41	61.2	765	2 Q6FPT7	Q6FPT7 candida gla
19	41	61.2	920	1 MML7_MYCTU	P96289 mycobacteri
20	41	61.2	999	2 Q7N1E3	Q7N1E3 glaucobacter
21	40	59.7	171	2 Q8HG38	Q8HG38 alligator s
22	40	59.7	205	2 Q6LOE6	Q6LOE6 picophylus
23	40	59.7	213	2 Q72S22	Q72S22 xenopus lae
24	40	59.7	232	1 CYSH_SYNP7	Q55309 synchococc
25	40	59.7	288	2 Q8KXW1	Q8KXW1 leucocostoc
26	40	59.7	288	2 CAD24411	CAD24411 leucocost
27	40	59.7	284	2 Q31016	Q31016 vibrio angu
28	40	59.7	322	1 FAH8_TROWT	Q83H15 tropheryma
29	40	59.7	462	2 Q8BRE3	Q8BRE3 mus musculu
30	40	59.7	492	2 Q9A7D4	Q9A7D4 caulobacter
31	40	59.7	555	2 Q754E9	Q754E9 ashyia goss

32	40	59.7	555	2 AAS53492	AAS53492 ashyia go
33	40	59.7	579	2 Q9KPJ7	Q9KPJ7 vibrio chol
34	40	59.7	623	2 Q7TMM1	Q7TMM1 mus musculu
35	40	59.7	681	2 Q8C751	Q8C751 mus musculu
36	40	59.7	681	2 Q8CFS2	Q8CFS2 mus musculu
37	40	59.7	745	2 Q86VR6	Q86VR6 homo sapien
38	40	59.7	826	2 Q9VX34	Q9VX34 drosophila
39	40	59.7	875	1 DD10_HUMAN	Q13306 homo sapien
40	40	59.7	891	2 Q80Y44	Q80Y44 mus musculu
41	40	59.7	1517	2 Q9SKV5	Q9SKV5 arabidopsis
42	39	58.2	111	2 Q92MB6	Q92MB6 rhizobium m
43	39	58.2	129	2 Q7R2L8	Q7R2L8 giardia lam
44	39	58.2	200	2 Q89DD4	Q89DD4 bradyrhizob
45	39	58.2	220	2 Q9ZKAS	Q9ZKAS helicobacte

ALIGNMENTS

RESULT 1					
ID	Q8U787	PRELIMINARY;	PRT;	382 AA.	
AC	Q8U787;				
DT	01-JUN-2002 (Tremblrel. 21, Created)				
DT	01-JUN-2002 (Tremblrel. 21, Last sequence update)				
DT	01-MAR-2004 (Tremblrel. 26, Last annotation update)				
DE	Transcriptional regulator, ROK family.				
GN	OrderedlocusNames=Atu4567;				
OC	Agrobacterium tumefaciens (strain C58 / ATCC 33970).				
OC	Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;				
OC	Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.				
OX	NCBI_Taxid=176299;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=Dupont;				
RA	MEDLINE=21608550; PubMed=11743193;				
RA	Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitaajima J.P.,				
RA	Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,				
RA	Chen Y., Paulsen I.T., Eissen J.A., Karp P.D., Bovee D. Sr.,				
RA	Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,				
RA	Kutyavlin T., Levy R., Li M.-J., McClelland E., Palmeri A.,				
RA	Ramond C., Rouse G., Saenphimachak C., Wu Z., Romero P., Gordon D.,				
RA	Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,				
RA	Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,				
RA	Chunley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,				
RT	Nester E.W.;				
RT	"The genome of the natural genetic engineer Agrobacterium tumefaciens				
RT	C58."				
RL	Science 294:2317-2323 (2001).				
DR	EMBL; AE009385; AAL45361.1; -.				
DR	PIR; AC3118; AC3118.				
DR	PIR; D98169; D98169.				
DR	InterPro; IPR000600; ROK.				
DR	InterPro; IPR009058; Wing_nlx_DNA_bnd.				
DR	Pfam; PF00480; ROK. 1.				
KW	Complete proteome.				
SQ	SEQUENCE 382 AA; 42285 MW; 77DP5DC2F279C20 CRC64;				
Query Match					
Best Local Similarity 80.0%; Pred. No. 22;					
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;					
QY	2 EFGAGLVGQ 11				
DB	226 EFGAGLVGQ 235				
RESULT 2					
ID	Q7CVA1	PRELIMINARY;	PRT;	402 AA.	
AC	Q7CVA1;				
DT	05-JUL-2004 (Tremblrel. 27, Created)				
DT	05-JUL-2004 (Tremblrel. 27, Last sequence update)				

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DT 05-JUL-2004 (TREMblrel. 27, Last annotation update)
DE AGR L 609p.
GN OrderedLocNames=AGR_L_609;
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
OX NCBI_TaxID=176299;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Cereon;
RX MEDLINE=21608551; PubMed=11743194;
RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
RA Houwillo B., Goldman B.S., Gao Y., Askenazi M., Halling C., Mullin L.,
RA Wollam C., Allinger M., Vaughn M., Iarchouk O., Epp A., Liu F.,
RA Flanagan C., Crowell C., Gursen J., Lomo C., Sear C., Strub G.,
RA Cielo C., Slater S.;
RT "Genome sequence of the plant pathogen and biotechnology agent
RT Agrobacterium tumefaciens C58."
RL Science 294:2323-2328(2001).
DR EMBL: AF008230; AKK8878.1; -.
DR InterPro: IPR000600; ROK.
DR InterPro: IPR009058; Wing_hlx_DNA_bnd.
DR Pfam: PF00480; ROK; 1.
SQ SEQUENCE 402 AA; 44410 MW; EF4426C3B616A820 CRC64;

Query Match      68.7%; Score 46; DB 2; Length 402;
Best Local Similarity 80.0%; Pred. No. 23;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 FEGAGLVGGQ 11
Db 246 FEGAGLVGGQ 255

RESULT 3
NIFT KLEBN
ID NIFT KLEBN STANDARD; PRT; 1171 AA.
AC P03833; P09112;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pyruvate-flavodoxin oxidoreductase (EC 1.2.7.-).
GN Name=niftj;
OS Klebsiella pneumoniae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Klebsiella.
OX NCBI_TaxID=573;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89094839; PubMed=1062178;
RA Arnold W., Rump A., Klipp W., Pfeifer U.B., Puehler A.;
RT "Nucleotide sequence of a 24,206-base-pair DNA fragment carrying the
RT entire nitrogen fixation gene cluster of Klebsiella pneumoniae."
RL J. Mol. Biol. 203:715-738(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=89083580; PubMed=3060860;
RA Cannon M., Cannon F., Buchanan-Mollaston V., Alley D., Alley A.,
RA Beynon J.;
RT "The nucleotide sequence of the nifH gene of Klebsiella pneumoniae."
RL Nucleic Acids Res. 16:11379-11379(1988).
RN [3]
RP REVISIONS, SEQUENCE FROM N.A.
RX MEDLINE=93247479; PubMed=8483412;
RA Charlton W., Cannon W., Buck M.;
RA "The Klebsiella pneumoniae nifH promoter: analysis of promoter
RT elements regulating activation by the NifA promoter."
RL Mol. Microbiol. 7:1007-1021(1993).
RN [4]
RP SEQUENCE OF 1-127 FROM N.A.
RX MEDLINE=83246546; PubMed=6306580;
RA Shen S., Xue Z., Kong Q., Wu Q.;

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RT "An open reading frame upstream from the nifH gene of Klebsiella
RT pneumoniae."
RL Nucleic Acids Res. 11:4241-4250(1983).
CC -1- FUNCTION: Oxidoreductase required for the transfer of electrons
CC from pyruvate to flavodoxin, which reduces nitrogenase.
CC -1- CATALYTIC ACTIVITY: Pyruvate + COA + oxidized flavodoxin = acetyl-
CC CoA + CO(2) + reduced flavodoxin.
CC -1- SIMILARITY: The iron-sulfur centers are similar to those of
CC bacterial-type 4Fe-4S ferredoxins.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
-----
DR EMBL: X01007; CA25502.1; -.
DR EMBL: X13303; CA31665.1; -.
DR EMBL: X13109; CA31501.1; -.
DR PIR: S01997; OOKBP.
DR HSSP: P94692; 1XKX.
DR InterPro: IPR001450; 4Fe4S_ferredoxin.
DR InterPro: IPR009051; Helical_ferredoxn.
DR InterPro: IPR002869; POR.
DR InterPro: IPR00399; Pyruvate decarb.
DR InterPro: IPR009014; Transketol_C-like.
DR Pfam: PF00037; Fer4_2.
DR Pfam: PF01558; POR_1.
DR Pfam: PF01855; POR_N_1.
DR Pfam: PF02775; TPP_enzyme_C_1.
DR PROSITE: PS00198; 4FE4S_FERREDOXIN; 2.
KW 4Fe-4S; Electron transport; Iron-sulfur; Nitrogen fixation;
KW Oxidoreductase.
FT METAL 691 691 Iron-sulfur 1 (4Fe-4S) (Potential).
FT METAL 694 694 Iron-sulfur 1 (4Fe-4S) (Potential).
FT METAL 697 697 Iron-sulfur 1 (4Fe-4S) (Potential).
FT METAL 701 701 Iron-sulfur 2 (4Fe-4S) (Potential).
FT METAL 745 745 Iron-sulfur 2 (4Fe-4S) (Potential).
FT METAL 748 748 Iron-sulfur 2 (4Fe-4S) (Potential).
FT METAL 751 751 Iron-sulfur 1 (4Fe-4S) (Potential).
FT METAL 755 755 Iron-sulfur 1 (4Fe-4S) (Potential).
FT CONFLICT 406 406 A -> R (in Ref. 2).
SQ SEQUENCE 1171 AA; 128041 MW; 95796232AD11012C CRC64;

Query Match      68.7%; Score 46; DB 1; Length 1171;
Best Local Similarity 72.7%; Pred. No. 60;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FEGAGLVGGQ 11
Db 873 FEGAGLVGGQ 883

RESULT 4
ID Q755M3 PRELIMINARY; PRT; 160 AA.
AC Q755M3;
DT 05-JUL-2004 (TREMblrel. 27, Created)
DT 05-JUL-2004 (TREMblrel. 27, Last sequence update)
DE 05-JUL-2004 (TREMblrel. 27, Last annotation update)
DE AFL2099Wp.
GN Name=AFL209Wp;
OS Ashbya gossypii (Yeast) (Bremothecium gossypii).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Bremothecium.
OX NCBI_TaxID=33169;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 10895;
RX PubMed=15001715;

```

RA Dietrich F.S., Voegelé S., Brachat S., Lerch A., Gates K., Steiner S.,
 RA Mohr C., Pohlmann R., Luedi P., Choi S., Wing R.A., Flavlier A.,
 RA Gaffney T.D., Philippen P.,
 RT "The Asbya gossypii genome as a tool for mapping the ancient
 RT Saccharomyces cerevisiae genome."
 RL Science 304:304-307(2004).
 DR EMBL: AE016899; AAS53165.1; -.
 DR AGD: AFL209W; -.
 SQ SEQUENCE 160 AA; 17720 MW; 38527868AB7B092E CRC64;

Query Match 62.7%; Score 42; DB 2; Length 160;
 Best Local Similarity 80.0%; Pred. No. 49;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 GAGLVGGGF 12
 DB 149 GAGTTLGGGF 158

RESULT 5
 AAS53165 PRELIMINARY; PRT; 160 AA.
 AC AAS53165;
 DT 23-APR-2004 (TrEMBLrel. 27, Created)
 DT 23-APR-2004 (TrEMBLrel. 27, Last sequence update)
 DT 23-APR-2004 (TrEMBLrel. 27, Last annotation update)
 DE AFL209WP.
 GN AFL209W.
 OS Asbya gossypii (Yeast) (Eremothecium gossypii).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Eremothecium.
 OX NCBI_TaxID=33169;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 10895;
 RX PubMed=15001715;
 RA Dietrich F.S., Voegelé S., Brachat S., Lerch A., Gates K., Steiner S.,
 RA Mohr C., Pohlmann R., Luedi P., Choi S., Wing R.A., Flavlier A.,
 RA Gaffney T.D., Philippen P.,
 RT "The Asbya gossypii genome as a tool for mapping the ancient
 RT Saccharomyces cerevisiae genome."
 RL Science 304:304-307(2004).
 DR EMBL: AE016899; AAS53165.1; -.
 SQ SEQUENCE 160 AA; 17720 MW; 38527868AB7B092E CRC64;

Query Match 62.7%; Score 42; DB 2; Length 160;
 Best Local Similarity 80.0%; Pred. No. 49;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 GAGLVGGGF 12
 DB 149 GAGTTLGGGF 158

RESULT 6
 O9RS23 PRELIMINARY; PRT; 396 AA.
 AC O9RS23;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAY-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein DR2304.
 GN OrderedLocusNames=DR2304;
 OS Deinococcus radiodurans.
 OC Deinococcus; Deinococcus-Thermus; Deinococci; Deinococcales;
 OC Deinococcaceae; Deinococcus.
 OX NCBI_TaxID=1299;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=R1 / ATCC 13939 / DSM 20539 / NCIB 9279;
 RX MEDLINE=20036896; PubMed=10567266;
 RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
 RA Dodson R.J., Haft D.H., Gwin M.L., Nelson W.C., Richardson D.L.,

RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
 RA Vamathevan J., Lam P., McDonald L.A., Uterback T.R., Zaleski C.,
 RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
 RA Ketchum K.A., Nelson K.E., Salzberg S.L., Smith H.O., Venter J.C.,
 RA Frazer C.W.;
 RT "Genome sequence of the radioresistant bacterium Deinococcus
 RT radiodurans R1."
 RL Science 286:1571-1577(1999).
 DR EMBL: AE002062; AAF11854.1; -.
 DR PIR: B75290; B75290.
 DR TIGR: DR2304; -.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 396 AA; 39229 MW; 355FCB5B0179F312 CRC64;

Query Match 62.7%; Score 42; DB 2; Length 396;
 Best Local Similarity 88.9%; Pred. No. 11e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 FGAGLVGG 10
 DB 264 FGAGFVLGG 272

RESULT 7
 O6CC56 PRELIMINARY; PRT; 540 AA.
 AC O6CC56;
 DT 01-OCT-2004 (TrEMBLrel. 28, Created)
 DT 01-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Chromosome C of strain CL1B99 of Yarrowia lipolytica.
 GN ORFNames=VAL10C12342g;
 OS Yarrowia lipolytica (Candida lipolytica).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Dipodascaceae; Yarrowia.
 OX NCBI_TaxID=4952;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CL1B99;
 RG GENOLEVRES;
 RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
 RA Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
 RA Goffard N., Frangeul L., Aigle M., Anhouard V., Babour A., Barbe V.,
 RA Barney S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
 RA Boerame A., Boyer J., Catolico L., Confanioli F., de Darvar A.,
 RA Despons L., Fabre B., Fairhead C., Ferry-Dunazet H., Groppi A.,
 RA Hantaye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
 RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
 RA Micaud J.M., Nikolski M., Ozaa S., Ozier-Kalogiropoulos O.,
 RA Pellenz S., Potier S., Richard G.F., Strub M.L., Suleau A.,
 RA Swennene D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
 RA Zenlou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
 RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
 RA "Genome evolution in yeasts."
 RL Nature 430:35-44(2004).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CL1B99;
 RA Genoscope;
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: CR382129; CAG82066.1; -.
 SQ SEQUENCE 540 AA; 58440 MW; BCC2AB595C981AF CRC64;

Query Match 62.7%; Score 42; DB 2; Length 540;
 Best Local Similarity 72.7%; Pred. No. 1.5e+02;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 EFGAGLVGGQ 11
 DB 342 EFGAKVLGGK 352

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RESULT 8
O92P15 PRELIMINARY; PRT; 155 AA.
ID O92P15
AC O92P15;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE HYDROTHERMAL TRANSMEMBRANE SIGNAL PEPTIDE PROTEIN.
GN OrderedlocusNames=R01982; ORFNames=SMC04336;
OS Rhizobium meliloti (Sinorhizobium meliloti);
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=21368234; PubMed=11474104;
RA Galibert F., Fian T.M., Long S.R., Puehler A., Abola P., Ampe F.,
RA Barloy-Hubler F., Barnett M.U., Becker A., Boistard P., Bothe G.,
RA Boutry M., Bowser L., Buhrmester J., Cadieu E., Capela D., Chain P.,
RA Cowie A., Davis R.W., Dreano S., Federspiel N.A., Fisher R.F.,
RA Gloux S., Godrie T., Goffeau A., Golding B., Gouzy J., Gurjal M.,
RA Hernandez-Lucas I., Hong A., Huizar L., Hyman R.W., Jones T., Kahn D.,
RA Kahn M.L., Kalman S., Keating D.H., Kiss E., Komp C., Lelaure V.,
RA Masny D., Palm C., Peck M.C., Pohl T.W., Portetelle D., Purnelle B.,
RA Ramsperger U., Surzycki R., Thebault P., Vandenbol M.,
RA Vorholter U.J., Weidner S., Wells D.H., Wong K., Yeh K.-C., Batut J.;
RT "The composite genome of the legume symbiont Sinorhizobium meliloti.";
RL Science 293:668-672(2001).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=2136507; PubMed=11481430;
RA Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
RA Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
RA Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masny D.,
RA Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U.,
RA Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;
RT "Analysis of the chromosome sequence of the legume symbiont
RT Sinorhizobium meliloti strain 1021.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
DR EMBL; AL591789; CAC46561.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
KM Complete proteome; Hypothetical protein; Transmembrane.
SQ SEQUENCE 155 AA; 17944 MW; 0A3E1286D1FDAFA CRC64;

Query Match 61.2%; Score 41; DB 2; Length 155;
Best Local Similarity 66.7%; Pred. No. 71;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Oy 2 FGAGVIVGG 10
Db 93 FGAGMITGG 101

RESULT 9
O84633 PRELIMINARY; PRT; 291 AA.
ID O84633
AC O84633;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Geranylgeranyl pyrophosphate synthase.
GN Name=19PA; OrderedlocusNames=CT628;
OS Chlamydia trachomatis;
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D / UM-3 / Cx;
RX MEDLINE=99000809; PubMed=9794136;
RA Stephens R.S., Kalman S., Lammel C.J., Fan J., Marache R., Aravind L.,
RA Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,

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RA Davis R.W.;
RT "Genome sequence of an obligate intracellular pathogen of humans:
RT Chlamydia trachomatis.";
RL Science 282:754-759(1998).
DR EMBL; AE001333; AAC68232.1; -.
DR PIR; E71491; E71491.
DR GO; GO:0008299; P:isoprenoid biosynthesis; IEA.
DR InterPro; IPR000092; Polyprenyl_synth.
DR InterPro; IPR008949; Terpenoid_synth.
DR Pfam; PF00348; Polyprenyl_synth; 1.
DR PROSITE; PS00723; POLYPRENYL_SYNTHET_1; 1.
DR PROSITE; PS00444; POLYPRENYL_SYNTHET_2; 1.
KM Complete proteome.
SQ SEQUENCE 291 AA; 32550 MW; C257BF3929D5F839 CRC64;

Query Match 61.2%; Score 41; DB 2; Length 291;
Best Local Similarity 63.6%; Pred. No. 1,2e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 2 FGAGVIVGGOF 12
Db 153 FGAGVIVGGOF 163

RESULT 10
ATX2 YEAST
ID ATX2 YEAST STANDARD; PRT; 313 AA.
AC 012067;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Metal homeostasis factor ATX2.
GN Name=ATX2; OrderedlocusNames=YOR079C; ORFNames=YOR29-30;
OS Saccharomyces cerevisiae (baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97042460; PubMed=8887660;
RA Lin S.-J., Culotta V.C.;
RT "Suppression of oxidative damage by Saccharomyces cerevisiae ATX2,
RT which encodes a manganese-traffic protein that localizes to Golgi-
RT like vesicles.";
RL Mol. Cell. Biol. 16:6303-6312(1996).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97279235; PubMed=9133743;
RA Valens M., Bonn C., Dalgman-Fornier B., Dang V., Bolotin-Fukuhara M.;
RT "The sequence of a 54.7 kb fragment of yeast chromosome XV reveals the
RT presence of two tRNAs and 24 new open reading frames.";
RL Yeast 13:379-390(1997).
CC -!- FUNCTION: Functions in the homeostasis of manganese ions.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Golgi.
CC
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DR EMBL; U46033; AAB37236.1; -.
DR EMBL; Z74987; CAA99272.1; -.
DR EMBL; Z70678; CAA94564.1; -.
DR PIR; S66962; S66962.
DR GeneOnline; 143667; -.
DR SGD; S0005605; ATX2.
DR GO; GO:0000139; C:Golgi membrane; IEA.
DR GO; GO:0005384; F:manganese ion transporter activity; IGI.
DR GO; GO:0030026; P:manganese ion homeostasis; IGI.
DR InterPro; IPR003689; Zn_transpt_Zip.

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DR Pfam; PF02535; 21p; 1.
 KW Golgi stack; Transmembrane.
 FT TRANSMEM 3 23 Potential.
 RT TRANSMEM 68 88 Potential.
 FT TRANSMEM 104 124 Potential.
 FT TRANSMEM 155 175 Potential.
 FT TRANSMEM 184 204 Potential.
 FT TRANSMEM 218 238 Potential.
 FT TRANSMEM 252 272 Potential.
 FT TRANSMEM 286 306 Potential.
 SQ SEQUENCE 313 AA; 34408 MW; 81DAEF0E4692268 CRC64;

Query Match 61.2%; Score 41; DB 1; Length 313;
 Best Local Similarity 53.8%; Pred. No. 1.3e+02;
 Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 EFGAGLVGGQFM 13
 DB 73 QFGIGMLTGTSPM 85

RESULT 11
 AAS56363 PRELIMINARY; PRT; 313 AA.
 ID AAS56363;
 AC AAS56363;
 DT 25-MAR-2004 (TREMBLrel. 27, Created)
 DT 25-MAR-2004 (TREMBLrel. 27, Last sequence update)
 DT 25-MAR-2004 (TREMBLrel. 27, Last annotation update)
 DE YOR079C.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC Saccharomycetales; Saccharomycetaceae; Saccharomycos.
 CX NCBI_TaxId=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Mareischky G., Rolfs A., Richardson A., Kane M., Bagui M., Taycher E.,
 RA Hu Y., Vanberg F., Weger J., Kramer J., Moreira D., Kelley F.,
 RA Zuo D., Raphael J., Hogle C., Jepson D., Williamson J., Camargo A.,
 RA Guoaga L., Vasconcelos A.T., Simpson A., Kolodner R., Harlow E.,
 RA Labber J.,
 RA "Creation of the YFLEX clone resource: cloning of Saccharomycos
 RT cerevisiae ORFs in the Gateway recombinational cloning system."
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY550637; AAS56363.1; -
 SQ SEQUENCE 313 AA; 34408 MW; 81DAEF0E4692268 CRC64;

Query Match 61.2%; Score 41; DB 2; Length 313;
 Best Local Similarity 53.8%; Pred. No. 1.3e+02;
 Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 EFGAGLVGGQFM 13
 DB 73 QFGIGMLTGTSPM 85

RESULT 12
 Q82N27 PRELIMINARY; PRT; 319 AA.
 ID Q82N27;
 AC Q82N27;
 DT 01-JUN-2003 (TREMBLrel. 24, Created)
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Putative sugar kinase.
 GN OrderedLocNames=SAV1476;
 OS Streptomyces avermitilis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 CC Streptomycinae; Streptomycetaceae; Streptomycos.
 CX NCBI_TaxId=33903;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MA-4680;
 RX MEDLINE=21477403; PubMed=11572948;
 RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,

RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osone T.,
 RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.,
 RT "Genome sequence of an industrial microorganism Streptomyces
 RT avermitilis: deducing the ability of producing secondary
 RT metabolites."
 RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MA-4680;
 RX MEDLINE=22608306; PubMed=12692562;
 RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
 RA Sakaki Y., Hattori M., Omura S.,
 RT "Complete genome sequence and comparative analysis of the industrial
 RT microorganism Streptomyces avermitilis."
 RL Nat. Biotechnol. 21:526-531(2003).
 DR EMBL: AP05027; BAC69186.1; -
 DR GO:0016301; P:kinase activity; IEA.
 DR InterPro: IPR006000; ROK.
 DR Pfam: PF00480; ROK; 1.
 DR PROSITE: PS01125; ROK; 1.
 KW Complete proteome; Kinase.
 SQ SEQUENCE 319 AA; 31301 MW; A0EEF6DA6A38FD29 CRC64;

Query Match 61.2%; Score 41; DB 2; Length 319;
 Best Local Similarity 88.9%; Pred. No. 1.3e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 GAGVLVGGQ 11
 DB 143 GGGVLVGGQ 151

RESULT 13
 Q6FWS6 PRELIMINARY; PRT; 331 AA.
 ID Q6FWS6;
 AC Q6FWS6;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Similar to gp[Q12067 Saccharomyces cerevisiae YOR079C Metal
 DE homeostasis factor.
 GN ORFNames=CAGL0K05577g;
 OS Candida glabrata (Yeast) (Torulopsis glabrata).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC Saccharomycetales; mitosporic Saccharomycetales; Candida.
 CX NCBI_TaxId=5478;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CBS138;
 RG GENOLEVURES;
 RA Dujon B., Sherman D., Fischer G., Durenne P., Casaregola S.,
 RA Lalontaine I., de Montigny J., Marc C., Nevegilise C., Talla E.,
 RA Goffard N., Frangoul L., Algle M., Anthonard V., Babbour A., Barbe V.,
 RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
 RA Boissiere A., Boyer J., Cattolico L., Confalonieri F., de Darvar A.,
 RA Despons L., Fabre E., Fairhead C., Ferry-Dunazet H., Groppi A.,
 RA Hantreay F., Hennequin C., Jauniaux N., Joyer P., Kachouri R.,
 RA Kerrest A., Koszul R., Lemaire M., Lezur I., Ma L., Muller H.,
 RA Niclaud J.M., Nikolski M., Oztas S., Ozier-Kalogiropoulos O.,
 RA Pellenn S., Polier S., Richard G.F., Strub M.L., Suleau A.,
 RA Swenne D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
 RA Zenlou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
 RA Bouchier C., Caudron B., Scarpelli C., Galliard C., Weisenbach J.,
 RA Wincker P., Souciet J.L.,
 RT "Genome evolution in yeasts."
 RL Nature 430:35-44(2004).
 DR EMBL: CR380957; CAG61429.1; -
 DR InterPro: IPR003689; Zn_transp_1p.
 DR Pfam: PF02535; 21p; 1.
 SQ SEQUENCE 331 AA; 36113 MW; F8337EFPDF1B0E0 CRC64;

Query Match 61.2%; Score 41; DB 2; Length 331;
 Best Local Similarity 53.8%; Pred. No. 1.4e+02;

Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EFGAGLVIGGQFM 13
 Db 49 QFGVGMILGTAFM 61

RESULT 14

Q916G8 PRELIMINARY; PRT; 347 AA.

AC Q916G8; 01-MAR-2001 (TEMBLrel. 16, Created)
 DT 01-MAR-2001 (TEMBLrel. 16, Last sequence update)
 DE 01-JUN-2003 (TEMBLrel. 24, Last annotation update)
 GN OrderedocNames=PA0323;
 OS Pseudomonas aeruginosa;
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas;
 NCBI_TaxID=287;
 [1] SEQUENCE FROM N.A.

RC STRAIN=ATCC 15692 / PA01;
 RX MEDLINE=20437337; Pubmed=10984043;
 RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
 RA Hickey M.J., Brinkman F.S.L., Huftagle W.O., Kowalik D.J., Lagrou M.,
 RA Garber R.L., Goltzy L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
 RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Paulsen M.V.;
 RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
 opportunistic pathogen."
 RL Nature 406:959-964(2000).
 DR EMBL: AE004470; AAG03712.1; -.
 DR PIR: D83605; D83605.
 DR HSSP: P31133; 1A99.
 DR GO: GO:0030288; C:periplasmic space (sensu Gram-negative Bact. .; IEA.
 DR GO: GO:0005215; F:transporter activity; IEA.
 DR GO: GO:0006810; P:transport; IEA.
 DR InterPro: IPR001188; SPTm/putr-bndng.
 DR Pfam: PF01847; SBP_bac.1; 1.
 DR PRINTS: PR00909; SPERMNDNDNG.
 KW Complete proteome.
 SQ SEQUENCE 347 AA; 38901 MW; 74B371F8684D183C CRC64;

Query Match 61.2%; Score 41; DB 2; Length 347;
 Best Local Similarity 80.0%; Pred. No. 1.5e+02;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 FGAAGLVIGGQ 11
 Db 11 FGAAGLVIGGQ 20

RESULT 15

Q74EW6 PRELIMINARY; PRT; 444 AA.

AC Q74EW6; 05-JUL-2004 (TEMBLrel. 27, Created)
 DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)
 DE 05-JUL-2004 (TEMBLrel. 27, Last annotation update)
 GN NADH oxidase, putative.
 OS ORFNames=GSU0843;
 OC Geobacter sulfurreducens.
 OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;
 OC Geobacteraceae; Geobacter.
 NCBI_TaxID=35554;
 [1] SEQUENCE FROM N.A.

RC STRAIN=PCA / ATCC 51573;
 RX Pubmed=14671304; DOI=10.1126/science.1088727;
 RA Mehe B.A., Nelson K.E., Eisen J.A., Paulsen I.T., Nelson W.C.,

RA Heidelberg J.F., Wu D., Wu M., Ward N.L., Beanan M.J., Dodson R.J.,
 RA Madupu R., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S.,
 RA Gwim M.L., Kolonay J.F., Sullivan S.A., Haft D.H., Selengut J.,
 RA Davidsen T.M., Zafar N., White O., Tran B., Romero C., Fordeger H.A.,
 RA Weidman J.F., Khouri H.M., Feldblyum T.V., Uterback T.R.,
 RA Van Aken S.E., Lovley D.R., Fraser C.M.;
 RT "Genome of Geobacter sulfurreducens: metal reduction in subsurface
 environments."
 RL Science 302:1967-1969(2003).
 DR EMBL: AE017180; AAR34173.1; -.
 DR TIGR: GSU0843; -.
 DR InterPro: IPR001327; PAD_pyr_redox.
 DR InterPro: IPR000103; Pyridine_redox_2.
 DR InterPro: IPR001100; Pyr_redox.
 DR InterPro: IPR004099; Pyr_redox_dim.
 DR Pfam: PF00070; Pyr_redox_1.
 DR Pfam: PF02852; Pyr_redox_dim_1.
 DR PRINTS: PR00368; FADPNR.
 DR PRINTS: PR00411; PNDRPTASEI.
 DR PRINTS: PR00469; PNDRPTASEII.
 SQ SEQUENCE 444 AA; 47967 MW; 8F86F154DC054C94 CRC64;

Query Match 61.2%; Score 41; DB 2; Length 444;
 Best Local Similarity 61.5%; Pred. No. 1.8e+02;
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EFGAGLVIGGQFM 13
 Db 378 EKGTGLLGQWV 390

RESULT 16

AAR34173 PRELIMINARY; PRT; 444 AA.

AC AAR34173; 02-MAR-2004 (TEMBLrel. 27, Created)
 DT 02-MAR-2004 (TEMBLrel. 27, Last sequence update)
 DE 02-MAR-2004 (TEMBLrel. 27, Last annotation update)
 GN NADH oxidase, putative.
 OS Geobacter sulfurreducens.
 OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;
 OC Geobacteraceae; Geobacter.
 NCBI_TaxID=35554;
 [1] SEQUENCE FROM N.A.

RC STRAIN=PCA / ATCC 51573;
 RX Pubmed=14671304;
 RA Mehe B.A., Nelson K.E., Eisen J.A., Paulsen I.T., Nelson W.C.,
 RA Heidelberg J.F., Wu D., Ward N.L., Beanan M.J., Dodson R.J.,
 RA Madupu R., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S.,
 RA Gwim M.L., Kolonay J.F., Sullivan S.A., Haft D.H., Selengut J.,
 RA Davidsen T.M., Zafar N., White O., Tran B., Romero C., Fordeger H.A.,
 RA Weidman J., Khouri H.M., Feldblyum T.V., Uterback T.R.,
 RA Van Aken S.E., Lovley D.R., Fraser C.M.;
 RT "Genome of Geobacter sulfurreducens: metal reduction in subsurface
 environments."
 RL Science 302:1967-1969(2003).
 DR EMBL: AE017209; AAR34173.1; -.
 DR TIGR: GSU0843; -.
 SQ SEQUENCE 444 AA; 47967 MW; 8F86F154DC054C94 CRC64;

Query Match 61.2%; Score 41; DB 2; Length 444;
 Best Local Similarity 61.5%; Pred. No. 1.8e+02;
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EFGAGLVIGGQFM 13
 Db 378 EKGTGLLGQWV 390

RESULT 17

YF83_YEAST

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ID YFE9 YEAST STANDARD; PRT; 623 AA.
AC P43554;
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
GN Hypothetical 70.3 kDa protein in ABR2-EMP47 intergenic region.
OS OrderedLocustNames=YFL049W.
OC Saccharomyces cerevisiae (Baker's Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycaceae;
OC NCBI_TaxID=4932;
RN RP SEQUENCE FROM N.A.
RX STRAIN=6288C / AB972;
RX MEDLINE=95400292; PubMed=7670463;
RA Murakami Y., Naitou M., Hagiwara H., Shibata T., Ozawa M.,
RA Sasanuma S.-I., Sasanuma M., Tsuchiya Y., Soeda E., Yokoyama K.,
RA Yamazaki M.-A., Tashiro H., Eki T.;
RT "Analysis of the nucleotide sequence of chromosome VI from
RT Saccharomyces cerevisiae."
RT Nucleic Acids Res. 23:261-268 (1995).
CC -1- SIMILARITY: TO YEAST NP16.
CC -----
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DR EMBL; D50617; BAA09192.1; -.
DR PIR; S56206; S56206.
DR Germonline; 140107; -.
DR SGD; S0001845; YFL049W.
DR GO; GO:0005634; C:nucleus; IDA.
KW Hypothetical protein.
SQ SEQUENCE 623 AA; 70275 MW; A8AC00CAC8F0ED0E CRC64;

Query Match 61.2%; Score 41; DB 1; Length 623;
Best Local Similarity 63.6%; Pred. No. 2.4e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 EFGAGLVLGSG 11
DB 194 EFGASVIAAGQ 204

RESULT 18
O6PPT7 PRELIMINARY; PRT; 765 AA.
AC O6PPT7;
DT 05-JUL-2004 (TRMBLrel. 27, Created)
DT 05-JUL-2004 (TRMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TRMBLrel. 27, Last annotation update)
DE Similar to sp|P20448 Saccharomyces cerevisiae YJL033W HCA4.
GN ORFNames=CAGL01045G.
OS Candida glabrata (Yeast) (Torulopsis glabrata).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OC NCBI_TaxID=5478;
RN RP SEQUENCE FROM N.A.
RX STRAIN=CBS138;
RG GENOLEVRES;
RA Dujon B., Sherman D., Fischer G., Durans P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,
RA Goffard N., Fringuel L., Aigle M., Anthonard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
RA Boissière A., Boyer J., Catolico L., Confalonieri F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Gropi A.,
RA Hantaye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Kozzul R., Lemaître M., Lœur I., Ma L., Müller H.,

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RA Nicaud J.M., Nikolski M., Oza S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
RA Swenne D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zenlou-Meyer M., Zivanovic I., Bojotin-Pukhara M., Thiery A.,
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissendach J.,
RA Wincker P., Souclet J.L.;
RT "Genome evolution in yeasts."
RT Nature 430:35-44 (2004).
RL EMBL; CR380956; CAG60704.1; -.
DR InterPro; IPR011410; DEAD_1.
DR InterPro; IPR011545; DEAD/DEAH_N.
DR InterPro; IPR000629; DEAD_box.
DR InterPro; IPR001650; Helicase_C.
DR Pfam; PF00270; DEAD; 1.
DR Pfam; PF00271; Helicase_C; 1.
DR SMART; SM00487; DEXDC; 1.
DR SMART; SM00490; HELIC; 1.
DR PROSITE; PS00039; DEAD ATP HELICASE; UNKNOWN 1.
DR ATP-binding; Helicase; Hydrolase.
SQ SEQUENCE 765 AA; 87380 MW; A0FDB5B79E63504B CRC64;

Query Match 61.2%; Score 41; DB 2; Length 765;
Best Local Similarity 63.6%; Pred. No. 2.9e+02;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 EFGAGLVLGSG 11
DB 141 QFSAGLVIGSK 151

RESULT 19
MML7 MYCTU STANDARD; PRT; 920 AA.
ID MML7 MYCTU
AC P96259;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Putative membrane protein mml7.
GN Name=mml7; OrderedLocustNames=Rv2942, MT3012, Mb2967;
GN ORFNames=MTCY24G1.07c;
OS Mycobacterium tuberculosis, and
OC Mycobacterium bovis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacteriineae; Mycobacteriaceae; Mycobacterium.
OC NCBI_TaxID=1773, 1765;
RN RP SEQUENCE FROM N.A.
RC SPECIES=M.tuberculosis; STRAIN=H37RV;
RX MEDLINE=98295987; PubMed=9634230; DOI=10.1038/31159;
RA Cole S.T., Broch R., Parkhill J., Garnier T., Churcher C.M.,
RA Harris D.E., Gordon S.V., Eigler K., Gas S., Barry C.E. III,
RA Tekala F., Badcock K., Basham D., Brown D., Chillingworth T.,
RA Connor R., Davies R.M., Devlin K., Fellwell T., Gentles S., Hamlin N.,
RA Holroyd S., Hornsby T., Jagsis K., Krogh A., McLean J., Moule S.,
RA Murphy L.D., Oliver S., Osborne J., Quail M.A., Rajandream M.A.,
RA Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrett B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence."
RL Nature 393:537-544 (1998).
RN RP SEQUENCE FROM N.A.
RC SPECIES=M.tuberculosis; STRAIN=CDC 1551 / Oshkosh;
RX MEDLINE=22206494; PubMed=12218036;
RA Fleischnann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J.D., Deboy R.T., Dodson R.J., Gwinn M.L., Haft D.H.,
RA Hickey B.K., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D.,
RA Salzberg S.L., Delcher A., Ustehack T.R., Weidman J.F., Khouri H.M.,
RA Gill J., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C.,
RA Fraser C.M.;
RT "Whole-genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains."
RL J. Bacteriol. 184:5479-5490 (2002).

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RN [3]
RP SPECIES=M.bovis; STRAIN=AP2122/97; DOI=10.1073/pnas.1130426100;
RC MEDLINE=22709107; PubMed=12786972;
RA Garnier T., Sigheleier K., Camus J.-C., Medina N., Mansoor H.,
RA Pryor M., Duchoy S., Grondin S., Lacroix C., Monsemp C., Simon S.,
RA Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
RA Parkhill J., Barrett B.G., Cole S.T., Gordon S.V., Hewinson R.G.,
RT "The complete genome sequence of Mycobacterium bovis."
RL Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- SIMILARITY: Belongs to the mmpL family.
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DR EMBL; BX842581; CAB06107.1; -
DR EMBL; AE007123; AA47339.1; -
DR EMBL; BX248344; CAD96654.1; -
DR TIGR; C70668; C70668.
DR TIGR; MT3012; -
DR Tuberculist; Rv2942; -
DR InterPro; IPR004869; MMP_L.
DR Pfam; PF03176; MMP_L; 1.
KM Complete proteome; Hypothetical protein; Transmembrane.
FT FT TRANSMEM 44 64 Potential.
FT TRANSMEM 210 230 Potential.
FT TRANSMEM 241 261 Potential.
FT TRANSMEM 271 291 Potential.
FT TRANSMEM 311 331 Potential.
FT TRANSMEM 344 364 Potential.
FT TRANSMEM 389 409 Potential.
FT TRANSMEM 761 781 Potential.
FT TRANSMEM 790 810 Potential.
FT TRANSMEM 822 842 Potential.
FT TRANSMEM 864 884 Potential.
FT TRANSMEM 920 940 Potential.
SQ SEQUENCE 920 AA; 95121 MW; 019FCA9294A854D2 CRC64;

Query Match
Best Local Similarity 61.2%; Score 41; DB 1; Length 920;
Matches 10; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

OY 2 FGAGLVV--GGQF 12
DB 876 FGAGLVVSGGSF 888

RESULT 20
O7NJE3 PRELIMINARY; PRT; 999 AA.
AC O7NJE3;
DT 01-MAR-2004 (TREMBlrel. 26, Created)
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
DE G11889 protein.
GN OrderedLocNames=G11889;
OS Gloeobacter violaceus.
OC Bacteria; Cyanobacteria; Chroococcales; Gloeobacter.
OX NCBI_TaxID=33072;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PCC 7421;
RX MEDLINE=22977040; PubMed=14621292;
RA Nakamura Y., Kaneko T., Sato S., Miura M., Miyashita H., Tsuchiya T.,
RA Sasamoto S., Watanabe A., Kawashima K., Kishida Y., Kiyokawa C.,
RA Kohara M., Matsumoto M., Matsuno A., Nakazaki N., Shimpo S.,
RA Takeuchi C., Yamada M., Tabata S.;

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RT "Complete genome structure of Gloeobacter violaceus PCC 7421, a
RT cyanobacterium that lacks thylakoids."
RL DNA Res. 10:137-145(2003).
DR EMBL; AP006574; BAC89830.1; -
DR GO; GO:0005871; C:kinesin complex; IEA.
DR GO; GO:0003777; F:microtubule motor activity; IEA.
DR InterPro; IPR002151; Kinesin_light.
DR InterPro; IPR001440; TPR.
DR Pfam; PF00515; TPR; 9.
DR PRINTS; PRO0381; KINESINLIGHT.
DR PROSITE; PS50005; TPR; 6.
DR PROSITE; PS50293; TPR_REGION; 1.
SQ Complete proteome.
KM SEQUENCE 999 AA; 109847 MW; ED9FA1239AB564B5 CRC64;

Query Match
Best Local Similarity 72.7%; Score 41; DB 2; Length 999;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 EFGAGLVG3Q 11
DB 901 EFGAGLVG3E 911

RESULT 21
O8HG38 PRELIMINARY; PRT; 171 AA.
AC O8HG38;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DE 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE NADH dehydrogenase subunit 6.
OS Alligator sinensis (Chinese alligator).
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Crocodylia; Alligatorine; Alligator.
OX NCBI_TaxID=38654;
RN [1]
RP SEQUENCE FROM N.A.
RA Wu X., Wang Y., Zhou K., Zhu W., Nie J., Wang C., Xie W.;
RL Submitted (May-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF511507; AAN84928.1; -
DR GO; GO:0005739; C:mitochondrion; IEA.
DR GO; GO:0008137; F:NADH dehydrogenase (ubiquinone) activity; IEA.
DR GO; GO:0006130; P:mitochondrial electron transport, NADH to u. .; IEA.
DR InterPro; IPR001457; Oxidored_g3.
DR Pfam; PF00499; Oxidored_g3; 1.
KM Mitochondrion.
SQ SEQUENCE 171 AA; 18603 MW; 51012386670F4FA3 CRC64;

Query Match
Best Local Similarity 59.7%; Score 40; DB 2; Length 171;
Matches 9; Conservative 2; Mismatches 1; Indels 2; Gaps 1;

OY 2 FGAGLVV--GGQFM 13
DB 37 FGAGLVVSGGSFM 50

RESULT 22
O6LOB6 PRELIMINARY; PRT; 205 AA.
AC O6LOB6;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE Translation initiation factor 2 beta subunit.
GN OrderedLocNames=PT00971;
OS Picrophilus torridus.
OC Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;
OC Picrophilaceae; Picrophilus.
OX NCBI_TaxID=82076;
RN [1]

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RP SEQUENCE FROM N.A.
 RC STRAIN=DSM 9790 / ATCC 700027;
 RA PubMed=15184674;
 RA Fueterer O., Angelov A., Liesegang H., Gottschalk G., Schleper C.,
 RA Schlegel B., Dock C., Antarakian G., Liebi W.,
 RT "Genome sequence of *Picrophilus torridus* and its implications for life
 RT around pH 0."
 RT Proc. Natl. Acad. Sci. U.S.A. 101:9091-9096(2004).
 RL EMBL, AB017261; AAT43556.1; -
 DR GO:0003743; F:translation initiation factor activity; IEA.
 DR InterPro: IPR002735; eIF5_eIF2B.
 DR InterPro: IPR002792; TRAM.
 DR Pfam: PF01873; eIF-5_eIF-2B; 1.
 DR Pfam: PF01938; TRAM; 1.
 DR Prodom: PD004078; eIF5_eIF2B; 1.
 DR SMART; SM00653; eIF2B_5; 1.
 DR PROSITE; PS50926; TRAM; 1.
 KW Complete proteome; Initiation factor.
 SQ SEQUENCE 205 AA; 23266 MW; 5BF3E104D64EA5C6 CRC64;
 Query Match 59.7%; Score 40; DB 2; Length 205;
 Best Local Similarity 72.7%; Pred. No. 1.3e+02;
 Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 EFGAGLVIGSQ 11
 DB 66 EFGAGLVIGSQ 76
 RESULT 23
 Q7S22 PRELIMINARY; PRT; 213 AA.
 AC Q7S22;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Claudin7L1 (MGC53400 protein).
 GN Name=cln7L1;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
 OC Xenopodidae; Xenopus.
 NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Fujita M., Itoh M., Shibata M., Taira S., Taira M.,
 RT "Gene expression pattern analysis of the tight junction protein,
 RT Claudin, in the early morphogenesis of *Xenopus* embryos."
 RT Gene Expr. Patterns 2:23-26(2002).
 RL [2]
 RN SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=23388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loughell N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richardson S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzyzanski M.I., Skalska U., Smalton D.E., Schermer A., Schein J.E.,
 RA Jones S.J., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=22341132; PubMed=12454917;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.,
 RT "Genetic and genomic tools for *Xenopus* research. The NIH *Xenopus*
 RT RT initiative."
 RT Dev. Dyn. 225:384-391(2002).
 RL [4]
 RN SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RA Klein S., Strausberg R.,
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL, AB072910; BAC21015.1; -
 DR EMBL, BC048771; AH48771.1; -
 DR GO:0016021; C:integral to membrane; IEA.
 DR GO:0005923; C:tight junction; IEA.
 DR GO:0005198; F:structural molecule activity; IEA.
 DR InterPro: IPR006187; Claudin.
 DR InterPro: IPR003552; Claudin7.
 DR InterPro: IPR006188; Claudin7.
 DR InterPro: IPR004031; PMP22_Claudin.
 DR Pfam: PF00822; PMP22_Claudin; 1.
 DR PRINTS; PR01077; CLAUDIN.
 DR PRINTS; PR01381; CLAUDIN7.
 DR PROSITE; PS01346; CLAUDIN; 1.
 KW Transmembrane.
 SQ SEQUENCE 213 AA; 22731 MW; CDDF3E2D804B5775 CRC64;
 Query Match 59.7%; Score 40; DB 2; Length 213;
 Best Local Similarity 60.0%; Pred. No. 1.4e+02;
 Matches 9; Conservative 2; Mismatches 2; Indels 2; Gaps 1;
 QY 1 EFGAGLVIG-GQFM 13
 DB 160 EFGAGLVIGMGMSFL 174
 RESULT 24
 CYSH_SYP7 STANDARD; PRT; 232 AA.
 ID CYSH_SYP7
 AC 055309; Q935X7;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Phosphoadenosine phosphosulfate reductase (EC 1.8.4.8) (PAPS
 DE reductase, thioredoxin dependent) (PAPs reductase) (3'-
 DE phosphoadenylylsulfate reductase) (PAPS sulfotransferase).
 GN Name=cysh; Synonyms=par, sea0019;
 OS *Synechococcus* sp. (strain PCC 7942) (Anacystis nidulans R2).
 OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
 NCBI_TaxID=1140;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9309269; PubMed=1463852;
 RA Niehaus A., Gieselmann G., Schenn J.D.,
 RT "Primary structure of the *Synechococcus* PCC 7942 PAPS reductase
 RT gene."
 RT Plant Mol. Biol. 20:1179-1183(1992).
 RL [2]
 RN SEQUENCE FROM N.A.
 RA Holtman C.K., Socias T., Mohler B.J., Chen Y., Min H., Golden S.S.,
 RA Yoderlin P.,
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Reduction of activated sulfate into sulfite.
 CC -1- CATALYTIC ACTIVITY: Adenosine 3',5'-bisphosphate + sulfite +
 CC oxidized thioredoxin = 3'-phosphoadenylyl sulfate + reduced
 CC thioredoxin.
 CC -1- PATHWAY: Sulfate activation; cysteine biosynthesis reductive
 CC branch; third step.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: Belongs to the PAPS reductase family. Cysh subfamily.

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 DR EMBL; M84476; AAA27328.1; -;
 DR EMBL; U30252; AAL03931.1; -;
 DR PIR; S28609; S28609.
 DR HSSP; P17854; ISUR.
 DR HAMAP; MF_00063; -; 1.
 DR InterPro; IPR004511; CysH.
 DR InterPro; IPR002500; PAPS_reduct.
 DR Pfam; PF01507; PAPS_reduct; 1.
 DR TIGRfams; TIGR00434; CysH; 1.
 KM Cysteine biosynthesis; Oxidoreductase.
 FT CONFLICT 218 218 T -> S (in Ref. 2).
 SQ SEQUENCE 232 AA; 26636 MW; 549FECB3BF8FD CRC64;

Query Match 59.7%; Score 40; DB 1; Length 232;
 Best Local Similarity 66.7%; Pred. No. 1.5e+02;
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EFGAGLVGGQF 12
 |||:||||
 Db 30 EFGAGLVGGQF 41

RESULT 25
 ID 08KMM1 PRELIMINARY; PRT; 288 AA.
 AC 08KMM1;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Putative fructokinase (EC 2.7.1.4).
 GN Name=fruk;
 OS Leuconostoc pseudomesenteroides.
 OC Bacteria; Firmicutes; Lactobacillales; Leuconostoc.
 NC NCBI_TaxID=33968;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATTC-12291;
 RA Helanto M.E.K., Airaksinen U., von Weymarn N., Leisola M.,
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ431694; CAD24411.4; -;
 DR GO; GO:000865; F:fructokinase activity; IEA.
 DR GO; GO:0016301; F:kinase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR InterPro; IPR006000; ROK.
 DR Pfam; PF00480; ROK; 1.
 DR PROSITE; PS01125; ROK; UNKNOWN_1.
 KM Kinase; Transferase.
 SQ SEQUENCE 288 AA; 31442 MW; F44974CFE8E953B1 CRC64;

Query Match 59.7%; Score 40; DB 2; Length 288;
 Best Local Similarity 63.6%; Pred. No. 1.8e+02;
 Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 GAGLVGGQFM 13
 |||:||||
 Db 136 GAGLVGGQFM 146

RESULT 26
 ID CAD24411 PRELIMINARY; PRT; 288 AA.
 AC CAD24411;
 DT 12-MAY-2004 (TrEMBLrel. 27, Created)
 DT 12-MAY-2004 (TrEMBLrel. 27, Last sequence update)

DT 12-MAY-2004 (TrEMBLrel. 27, Last annotation update)
 DE Putative fructokinase (EC 2.7.1.4).
 GN FRUK.
 OS Leuconostoc pseudomesenteroides.
 OC Bacteria; Firmicutes; Lactobacillales; Leuconostoc.
 NC NCBI_TaxID=33968;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATTC-12291;
 RA Helanto M.E.K., Airaksinen U., von Weymarn N., Leisola M.,
 RT "Characterization of random mutant strain of Leuconostoc
 RT pseudomesenteroides that cannot grow on fructose and its use in
 RT mannitol production."
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ431694; CAD24411.4; -;
 KM Kinase; Transferase.
 SQ SEQUENCE 288 AA; 31442 MW; F44974CFE8E953B1 CRC64;

Query Match 59.7%; Score 40; DB 2; Length 288;
 Best Local Similarity 63.6%; Pred. No. 1.8e+02;
 Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 GAGLVGGQFM 13
 |||:||||
 Db 136 GAGLVGGQFM 146

RESULT 27
 ID 031016 PRELIMINARY; PRT; 294 AA.
 AC 031016;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Putative rhamnosyl transferase.
 GN Name=orf33x8;
 OS Vibrio anguillarum (Listonella anguillarum).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; Listonella.
 NC NCBI_TaxID=55601;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=85-3954-2;
 RA Jedani K.E., Stroemer U.H., Manning P.A.,
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF025396; AAB81635.1; -;
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR InterPro; IPR001173; Glyco_trans_2.
 DR InterPro; IPR006446; Rhamnosyltran.
 DR Pfam; PF00535; Glycos_transf_2; 1.
 DR TIGRfams; TIGR01556; Rhamnosyltran; 1.
 KM Transferase.
 SQ SEQUENCE 294 AA; 33782 MW; 7ABC8A43467CB02C CRC64;

Query Match 59.7%; Score 40; DB 2; Length 294;
 Best Local Similarity 58.3%; Pred. No. 1.9e+02;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 EFGAGLVGGQF 12
 |||:||||
 Db 111 EFGAGLVGGQF 122

RESULT 28
 ID FASH_TROWT STANDARD; PRT; 322 AA.
 AC 083HL5; Q83N01;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 05-JUN-2004 (Rel. 44, Last annotation update)
 DE 3-oxoacyl-(acyl-carrier-protein) synthase III (EC 2.3.1.41) (Beta-
 DE ketoacyl-ACP synthase III) (KAS III).
 GN Name=fash; OrderedLocustNames=TW1253, TW517;

OS Tropheryma whipplei (strain Twist) (Whipple's bacillus), and
 OS Tropheryma whipplei (strain TW08/27) (Whipple's bacillus).
 OC Bacteria: Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Micrococcineae; Cellulomonadaceae; Tropheryma.
 RX NCB1_TaxID=203267, 218496;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=Twist / Genotype 2A;
 RX MEDLINE=22784088; PubMed=12902375; DOI=10.1101/gr.1474603;
 RA Raoult D., Ogata H., Audic S., Robert C., Suren K., Drancourt M.,
 RA Claverie J.-M.;
 RA "Tropheryma whipplei Twist: a human pathogenic Actinobacteria with a
 RT reduced genome.";
 RL Genome Res. 13:1800-1809(2003).
 RN (2)
 RP SEQUENCE FROM N.A.
 RC STRAIN=TW08/27;
 RX MEDLINE=22495039; PubMed=12606174;
 RA Bentley S.D., Mawhood M., Murphy L.D., Pallen M.J., Yeats C.A.,
 RA Dover L.G., Norbertczak H.T., Besra G.S., Quail M.A., Harris D.E.,
 RA von Herbay A., Goble A., Rutter S., Squares R., Squares S.,
 RA Barrell B.G., Parkhill J., Rellman D.A.;
 RA "Sequencing and analysis of the genome of the Whipple's disease
 RT bacterium Tropheryma whipplei.";
 RL Lancet 361:637-644(2003).
 RN (3)
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;
 RX MEDLINE=21085660; PubMed=11217851;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN (4)
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;
 RX MEDLINE=20499374; PubMed=11042159;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Kono H., Okazaki Y., Miyamatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN (5)
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;
 RX MEDLINE=20530913; PubMed=11076861;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Kono H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe K.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka K., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN (6)
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;
 RX MEDLINE=20530913; PubMed=11076861;
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Haeizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Kondo M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohnishi N., Okazaki Y.,

RESULT 29
 ID 08BRE3 PRELIMINARY; PRT; 462 AA.
 AC 08BRE3;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Mus musculus 9.5 days embryo parthenogenote cDNA, RIKEN full-length
 DE enriched library, clone: B130020M16 product: DEAD/H (Asp-Glu-Ala-
 DE Asp/His) box polypeptide 10 (RNA helicase), full insert sequence.
 DE (Fragment).
 GN Name=DDx10;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCB1_TaxID=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;
 RX MEDLINE=99279253; PubMed=10349636;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44(1999).
 RN (2)
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;
 RX MEDLINE=21085660; PubMed=11217851;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN (3)
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;
 RX MEDLINE=20499374; PubMed=11042159;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Kono H., Okazaki Y., Miyamatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN (5)
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;
 RX MEDLINE=20530913; PubMed=11076861;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Kono H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe K.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka K., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN (6)
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;
 RX MEDLINE=20530913; PubMed=11076861;
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Haeizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Kondo M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohnishi N., Okazaki Y.,

Query Match 59.7%; Score 40; DB 1; Length 322;
 Best Local Similarity 80.0%; Pred. No. 2e+02;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

2 FGAGLVGQ 11
 308 FGAGLVGQ 317

RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akashira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toy T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the DEAD box helicase family.
 CC EMBL: AK045032; BAC32191.1; -.
 DR MGD; MGI:1924841; Ddx10.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0008026; F:ATP-dependent helicase activity; IEA.
 DR GO; GO:0016787; F:Hydrolase activity; IEA.
 DR GO; GO:0003676; F:Nucleic acid binding; IEA.
 DR InterPro; IPR001410; DEAD.
 DR InterPro; IPR011545; DEAD/DEAH_N.
 DR InterPro; IPR000629; DEAD_box.
 DR InterPro; IPR001650; Helicase_C.
 DR Pfam; PF002270; DEAD_1.
 DR Pfam; PF002271; Helicase_C_1.
 DR SMART; SM00487; DEXDC_1.
 DR SMART; SM00490; HELIC_C_1.
 DR PROSITE; PS00039; DEAD_ATP_HELICASE; 1.
 KW ATP-binding; Helicase; Hydrolase.
 FT NON TER 462 462
 SQ SEQUENCE 462 AA; 53099 MW; A3F94D2A15FE645 CRC64;

Query Match 59.7%; Score 40; DB 2; Length 462;
 Best Local Similarity 54.5%; Pred. No. 2.8e+02;
 Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 EFGAGLVGCG 11
 DB 169 DFSAGLIIGK 179

RESULT 30
 ID 09A7D4

09A7D4 PRELIMINARY; PRT; 492 AA.

AC 09A7D4; 01-JUN-2001 (TRENBLREL. 17, Created)
 DT 01-JUN-2001 (TRENBLREL. 17, Last sequence update)
 DT 01-JUN-2003 (TRENBLREL. 24, Last annotation update)
 DE Hypothetical protein CCI1789.
 GN OrderedLocustNames=CCI1789;
 OS Caulobacter crescentus.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
 OC Caulobacteraceae; Caulobacter.
 OX NCBI_TaxID=155892;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 19089 / CB15;
 RX MEDLINE=21173698; PubMed=11259647; DOI=10.1073/pnas.061029298;
 RA Nietman W.C., Feilblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
 RA Eissen J.A., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
 RA Potocka I., Nelson W.C., Newton A., Stephens C., Phade N.D., Ely B.,
 RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
 RA Kolony J.F., Smit J., Craven M.B., Khoult H.M., Shetty J.,
 RA Berry K.J., Uterback T.R., Tran K., Wolf A.M., Vamathevan J.J.,
 RA Ermoiaeva M.D., White O., Salzberg S.L., Venter J.C., Shapiro L.,
 RA Frazer C.M.;
 RT "Complete genome sequence of Caulobacter crescentus."
 RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
 DR EMBL; AE005853; AAK23765.1; -.
 DR PIR; A87471; A87471.
 DR TIGR; CCI1789; -.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 492 AA; 52155 MW; 1AC33E2A9050D5A CRC64;

Query Match 59.7%; Score 40; DB 2; Length 492;
 Best Local Similarity 77.8%; Pred. No. 2.9e+02;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 EFGAGLVGCG 10
 DB 2 EFGAGLVGCG 10

DB 93 EFGAGLVGCG 101

RESULT 31

ID 0754E9 PRELIMINARY; PRT; 555 AA.

AC 0754E9; 05-JUL-2004 (TRENBLREL. 27, Created)
 DT 05-JUL-2004 (TRENBLREL. 27, Last sequence update)
 DT 05-JUL-2004 (TRENBLREL. 27, Last annotation update)
 DE AFR121WP.
 GN Name=AFR121W;
 OS Ashbya gossypii (Yeast) (Eremothecium gossypii).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Eremothecium.
 OX NCBI_TaxID=33169;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 10895;
 RX PubMed=15001715;
 RA Dietrich F.S., Voegelé S., Brachat S., Lerch A., Gates K., Steiner S.,
 RA Mohr C., Pohlmann R., Luedi P., Choi S., Wing R.A., Flavier A.,
 RA Gaffney T.D., Philippsen P.;
 RT "The Ashbya gossypii genome as a tool for mapping the ancient
 Saccharomyces cerevisiae genome."
 RL Science 304:304-307(2004).
 DR EMBL; AE016901; AAS53492.1; -.
 DR AGD; AFR121W; -.
 SQ SEQUENCE 555 AA; 65009 MW; 77A6D92DD6AFE3B8 CRC64;

Query Match 59.7%; Score 40; DB 2; Length 555;
 Best Local Similarity 61.5%; Pred. No. 3.3e+02;
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 EFGAGLVGCGFM 13
 DB 38 EFVKGRIIGNQM 50

RESULT 32

ID AAS53492 PRELIMINARY; PRT; 555 AA.

AC AAS53492; 23-APR-2004 (TRENBLREL. 27, Created)
 DT 23-APR-2004 (TRENBLREL. 27, Last sequence update)
 DT 23-APR-2004 (TRENBLREL. 27, Last annotation update)
 DE AFR121WP.
 GN AFR121W.
 OS Ashbya gossypii (Yeast) (Eremothecium gossypii).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Eremothecium.
 OX NCBI_TaxID=33169;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 10895;
 RX PubMed=15001715;
 RA Dietrich F.S., Voegelé S., Brachat S., Lerch A., Gates K., Steiner S.,
 RA Mohr C., Pohlmann R., Luedi P., Choi S., Wing R.A., Flavier A.,
 RA Gaffney T.D., Philippsen P.;
 RT "The Ashbya gossypii genome as a tool for mapping the ancient
 Saccharomyces cerevisiae genome."
 RL Science 304:304-307(2004).
 DR EMBL; AE016901; AAS53492.1; -.
 DR EMBL; AE016901; AAS53492.1; -.
 SQ SEQUENCE 555 AA; 65009 MW; 77A6D92DD6AFE3B8 CRC64;

Query Match 59.7%; Score 40; DB 2; Length 555;
 Best Local Similarity 61.5%; Pred. No. 3.3e+02;
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 EFGAGLVGCGFM 13
 DB 38 EFVKGRIIGNQM 50


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RESULT 33
09K9J7 PRELIMINARY; PRT; 579 AA.
ID 09K9J7;
AC 09K9J7;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Sensory box/GGDEF family protein.
GN OrderedLocusNames=VC2370;
OS Vibrato cholerae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrrio.
OX NCBI_TaxId=666;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=E1 Tor N16961 / Serotype O1;
RX MEDLINE=20406833; PubMed=10952301; DOI=10.1038/35020000;
RA Heidelberg J.F., Eisen J.A., Nelson M.C., Clayton R.A., Gwim M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.L.,
RA Ermolaeva M.D., Vamathevan J.J., Babs S., Qin H., Dragoi I.,
RA Sellers P., McDonald L.A., Utterback T.R., Fleischmann R.D.,
RA Nierman W.C., White O., Salzberg S.L., Smith H.O., Colwell R.R.,
RA Mekalanos J.J., Venter J.C., Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT cholerae."
RL Nature 406:477-483(2000).
DR EMBL; AE004307; AAF95513.1; -.
DR PIR; B82085; B82085.
DR TIGR; VC2370; -.
DR GO; GO:0000155; P:two-component sensor molecule activity; IEA.
DR GO; GO:0000160; P:two-component signal transduction system (p. . .); IEA.
DR InterPro; IPR001610; PAC.
DR InterPro; IPR001610; PAC.
DR InterPro; IPR000014; PAS.
DR InterPro; IPR000700; PAS-associat_C.
DR Pfam; PF00785; PAC; 1.
DR Pfam; PF00785; PAC; 1.
DR SMART; SM00267; DUF1.1.
DR SMART; SM00086; PAC; 2.
DR SMART; SM00091; PAS; 2.
DR TIGRfam; TIGR00254; GGDEF; 1.
DR TIGRfam; TIGR00229; sensory_box; 1.
DR PROSITE; PS50887; GGDEF; 1.
DR PROSITE; PS50113; PAC; 2.
DR Complete proteome.
SQ SEQUENCE 579 AA; 65762 MW; 6E37C8B467A46CD6 CRC64;

Query Match 59.7%; Score 40; DB 2; Length 579;
Best Local Similarity 88.9%; Pred. No. 3.4e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 FGAGLVGCG 10
Db 13 FGAGLVGCG 21

RESULT 34
07TMM1 PRELIMINARY; PRT; 623 AA.
ID 07TMM1;
AC 07TMM1;
DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Ddx10 protein (Fragment).
GN Name=Ddx10;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN (1)
RP SEQUENCE FROM N.A.

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RC STRAIN=FVB/N;
RC TISSUE=Mammary tumor. Metallothionein-TGF alpha model. 10 month old
RC virgin mouse. Taken by biopsy.
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo W.P., Caesavert T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman W., Madan A., Rodriguez P., Bouffard G.G.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywicki M.I., Skalska U., Smailus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN (2)
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N;
RC TISSUE=Mammary tumor. Metallothionein-TGF alpha model. 10 month old
RC virgin mouse. Taken by biopsy.
RX Strausberg R.;
RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the DEAD box helicase family.
DR EMBL; BC055481; AAH55481.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0008026; F:ATP-dependent helicase activity; IEA.
DR GO; GO:0016787; F:hydrolyase activity; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR01410; DEAD.
DR InterPro; IPR01545; DEAD/DEAH_N.
DR InterPro; IPR00629; DEAD-box.
DR InterPro; IPR01650; Helicase_C.
DR Pfam; PF00270; DEAD; 1.
DR Pfam; PF00271; Helicase_C; 1.
DR SMART; SM00487; DEXDC; 1.
DR SMART; SM00490; HELIC; 1.
DR PROSITE; PS00039; DEAD_ATP_HELICASE; 1.
DR ATP-binding; Helicase; Hydrolase.
FT NON TER 1 1
FT NON TER 623 623
SQ SEQUENCE 623 AA; 70849 MW; F5B6893E71179D94 CRC64;

Query Match 59.7%; Score 40; DB 2; Length 623;
Best Local Similarity 54.5%; Pred. No. 3.6e+02;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 ERGAGLVGCG 11
Db 111 ERGAGLVGCG 121

RESULT 35
08C751 PRELIMINARY; PRT; 681 AA.
ID 08C751;
AC 08C751;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Mus musculus 13 days embryo lung cDNA, RIKEN full-length enriched
DE library, clone:ID430047D13 product:DEAD/H (Aap-Glu-Ala-Asp/His) box
DE polypeptide 10 (RNA helicase), full insert sequence. (Fragment).
GN Name=Ddx10;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

NC Mmmap11a; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NGBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Lung;
RC MEDLINE=99279253; PubMed=10349636;
RX Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Lung;
RC MEDLINE=21085660; PubMed=11217851;
RX RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Lung;
RC The FANTOM Consortium,
RA The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RL 60,770 full-length cDNAs.";
RN Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Lung;
RC MEDLINE=20499374; PubMed=11042159;
RX Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Komori H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RL prepare full-length cDNA libraries for rapid discovery of new genes.";
RN Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Lung;
RC MEDLINE=20530913; PubMed=11076861;
RX Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
RA Komori H., Akiyama Y., Nishi K., Kiteunai T., Taahiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kasahagi K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Wataniki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsubara S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RL sequencing pipeline with 384 multicapillary sequencer.";
RN Genome Res. 10:1157-1171(2000).
RN [6]
RP SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Lung;
RC Adachi T., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai T., Kojima Y., Kondo S., Komori H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata N., Nakamura M.,
RA Nishi K., Nomura K., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Saito R., Satoh H., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tanaka T.,
RA Tomaru A., Toyata T., Yasunishi A., Takaki-Akahira S., Takeda Y., Tanaka T.,
RC Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SMILIARITY: Belongs to the DEAD box helicase family.
DR EMBL: AK052540; BAC3501.1; -
DR MGD: MGI:1924841; Ddx10.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0008026; F:ATP-dependent helicase activity; IEA.
DR GO: GO:0016787; F:Hydrolase activity; IEA.
DR GO: GO:0003676; F:Nucleic acid binding; IEA.
DR InterPro: IPR001410; DEAD.
DR InterPro: IPR011545; DEAD/DEAH_N.
DR InterPro: IPR000629; DEAD box.
DR InterPro: IPR001650; Helicase_C.

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DR Pfam; PF002270; DEAD; 1.
DR Pfam; PF002271; Helicase_C; 1.
DR SMART; SM00487; DEXDC; 1.
DR SMART; SM00490; HELICC; 1.
DR PROSITE; PS00039; DEAD_ATP_HELICASE; 1.
KW ATP-binding; Helicase; Hydrolase.
KW NON TER 681
FT SEQUENCE 681 AA; 77839 MW; EF86EB62BB6F988 CRC64;
SQ

Query Match 59.7%; Score 40; DB 2; Length 681;
Best Local Similarity 54.5%; Pred. No. 3.9e+02;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Db 169 DFGAGLITGK 179

QY 1 EFGAGLVAGQ 11
:|::|::|:
Db 169 DFGAGLITGK 179

RESULT 36
O8CFSS2 PRELIMINARY; PRT; 681 AA.
AC O8CFSS2;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Ddx10 protein (Fragment).
GN Name=Ddx10;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TTSUSE=Eye;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buecaw K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marutina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Carninci P., Frange C.,
RA Brownstein M., Ustin T.B., Toshiyuki S., Carninci P., Mullany S.J.,
RA Raha S.S., Loggani N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Gibbs R.A.,
RA Vialleton D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Halton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchan J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
RA Krzywnicki M.I., Skalska U., Smalins D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Mairia M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TTSUSE=Eye;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the DEAD box helicase family.
DR EMBL; BC023303; AAH23303.1; -.
DR HSSP; P10081; 10VA.
DR MGP; MGI-1924841; Ddx10.
DR GO; GO:0005524; P:ATP binding; IEA.
DR GO; GO:0008026; F:ATP-dependent helicase activity; IEA.
DR GO; GO:0016787; F:Hydrolase activity; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR001410; DEAD.
DR InterPro; IPR011545; DEAD/DEAH_N.
DR InterPro; IPR000629; DEAD box_1.
DR Pfam; PF00270; DEAD; 1.

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DR Pfam; PF00271; Helicase_C; 1.
 DR SMART; SM00487; DEXDC; 1.
 DR SMART; SM00490; HELIC; 1.
 DR PROSITE; PS00039; DEAD_ATP_HELICASE; 1.
 KM ATP-binding; Helicase; Hydrolase.
 FT NON_TER 681
 SQ SEQUENCE 681 AA; 77877 MW; E79A1870E68FC240 CRC64;

Query Match
 Best Local Similarity 59.7%; Score 40; DB 2; Length 681;
 Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EFGAGLVLCGQ 11
 Db 169 DFGAGLVLCGK 179

RESULT 37
 ID 086VR6 PRELIMINARY; PRT; 745 AA.
 AC 086VR6:
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DE DDX10 protein (Fragment).
 GN Name-DDX10;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymph;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strusberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mallary S.J.,
 RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skala U., Smalls D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Mitra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymph;
 RA Strusberg R.;
 RL Submitted (Mar-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the DEAD box helicase family.
 DR EMBL; BC049217; AAH49217.1; -;
 DR GO; GO:000524; F:ATP binding; IEA;
 DR GO; GO:0008026; F:ATP-dependent helicase activity; IEA;
 DR GO; GO:0016787; F:hydrolase activity; IEA;
 DR GO; GO:003676; F:nucleic acid binding; IEA;
 DR InterPro; IPR001410; DEAD;
 DR InterPro; IPR011545; DEAD/DEAH_N;
 DR InterPro; IPR000639; DEAD box;
 DR InterPro; IPR001650; Helicase_C;
 DR Pfam; PF00270; DEAD; 1;
 DR Pfam; PF00271; Helicase_C; 1;
 DR SMART; SM00487; DEXDC; 1;
 DR SMART; SM00490; HELIC; 1;

DR PROSITE; PS00039; DEAD_ATP_HELICASE; 1.
 KM ATP-binding; Helicase; Hydrolase.
 FT NON_TER 745
 SQ SEQUENCE 745 AA; 85831 MW; F689A0379D1C09CB CRC64;

Query Match
 Best Local Similarity 54.5%; Score 40; DB 2; Length 745;
 Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EFGAGLVLCGQ 11
 Db 169 DFGAGLVLCGK 179

RESULT 38
 ID 09VX34 PRELIMINARY; PRT; 826 AA.
 AC 09VX34;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE CG5800-PA (R619835P).
 GN ORFNames=CG5800;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H., Blaise R.G., Champagne M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
 RA Abail J.F., Aghayani A., An H.J., Andrews-Pfankuch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktoglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhattacharya P., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadiou E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegam C.,
 RA Jatali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laske P., Lei Y., Levitsky A.C., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Morkulov G., Mlshina N.V., Mobarry C., Morris J., Mostreft A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusslein D.R., Pauley J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puti V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.Y., Wasearan D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodgett, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhou W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=22426065; PubMed=12537568;
 RX Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,

RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
 RA George R.A., Hoekins R.A., Lavery T., Muzny D.M., Nelson C.R.,
 RA Patel J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 RA Svirkas R., Taber P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,
 RA "Finishing a whole-genome shotgun: release 3 of the Drosophila
 RT melanogaster euchromatic genome sequence."
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079 (2002).
 RN [3]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=22426070. PubMed=12537573;
 RX Kaminler J.S., Bergman C.M., Krommiller B., Carlson J., Svirkas R.,
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celniker S.E.;
 RT "The transposable elements of the Drosophila melanogaster euchromatin:
 RL a genomics perspective."
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084 (2002).
 RN [4]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=22426069. PubMed=12537572;
 RX Miura S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminler J.S., Millburn G.H., Prochuk S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu I., Berman B.P.,
 RA Belencont B.R., Celniker S.E., de Grey A.D., Drysdale K.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a
 RL systematic review."
 RL Genome Biol. 3:RESEARCH0083-RESEARCH0083 (2002).
 RN [5]
 RN SEQUENCE FROM N.A.
 RP FLYBASE;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RN SEQUENCE FROM N.A.
 RP FLYBASE;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RN SEQUENCE FROM N.A.
 RP STRAIN=Berkley;
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Dresnek D., Fattan D., Frise E.,
 RA George R., Gonzalez M., Guerin H., Krommiller B., Li P., Liao G.,
 RA Miranda A., Mungall C.J., Nuno J., Patel J., Paragas V., Park S.,
 RA Patel S., Phoonanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
 RA Celniker S.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AB003506; AAF48747.2; -;
 DR EMBL; AY119628; AAM50282.1; -;
 DR HSPF; F10081; 10DE.
 DR FLYBASE; FBgn0030855; CG5800.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0008026; F:ATP-dependent helicase activity; IEA.
 DR GO; GO:0003676; F:Nucleic acid binding; IEA.
 DR InterPro; IPR001410; DEAD.
 DR InterPro; IPR011545; DEAD/DEAH_N.
 DR InterPro; IPR000629; DEAD_box.
 DR InterPro; IPR001650; Helicase_C.
 DR Pfam; PF00270; DEAD; 1.
 DR Pfam; PF00271; Helicase_C; 1.
 DR SMART; SM00487; DEXDC; 1.
 DR SMART; SM00490; HELIC; 1.
 DR PROSITE; PS00039; DEAD_ATP_HELICASE; UNKNOWN_1.
 DR ATP-binding; Helicase; Hydrolase.
 SQ SEQUENCE 826 AA, 92844 MW, 92A2897054268066 CRC64;

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Db      172 DFSAGLITGK 182

RESULT 39
ID10_HUMAN DD10_HUMAN STANDARD; PRT; 875 AA.
AC Q13206;
DT 15-JUL-1998 (Rel. 36, Created)
DT 05-JUL-1998 (Rel. 36, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Probable ATP-dependent RNA helicase DDX10 (DEAD-box protein 10).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96301396; PubMed=8660968;
RA Savitsky K., Ziv Y., Bar-Shira A., Gilad S., Tagle D.A., Smith S.,
RA Uziel T., Sfez S., Nahmias J., Sartiel A., Eddy R.L., Shows T.B.,
RA Collins F.S., Shiloh Y., Rotman G.;
RT "A human gene (DDX10) encoding a putative DEAD-box RNA helicase at
RT 11q22-q23.";
RL Genomics 33:199-206(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Arai Y., Kaneo Y., Kubo T., Arai K., Hosoda F., Ohki M.;
RT "Molecular analysis of the chromosomal breakpoints and identification
RT of the repetitive sequences near the breakpoints of NUP98 in therapy-
RT related leukemia with inv(11)(p15q22).";
RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
CC -!- FUNCTION: Putative ATP-dependent RNA helicase.
CC -!- TISSUE SPECIFICITY: High in testis but widely expressed.
CC -!- SIMILARITY: Belongs to the DEAD box helicase family. DBP4/DDX10
CC subfamily.
CC -!- DATABASE: NAME=Atlas Genet. Cyto genet. Oncol. Haematol.;
CC WWW="http://www.infobiogen.fr/services/chromocancer/gene/DDX10.html".
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.ebi.ac.uk/announcements
CC or send an email to license@ebi.ac.uk).
CC -----
CC EMBL, U28042; AAC50823.1; -.
CC EMBL, AB040537; BAB18536.1; -.
CC HSSP: P10081; LOVA.
CC SWISS-2DPAGE: Q13206; HUMAN.
CC Genew; HGNC:2735; DDX10.
DR MIM: 601235; -.
DR GO: 0003724; F:RNA helicase activity; TAS.
DR InterPro: IPR001410; DEAD.
DR InterPro: IPR000629; DEAD_box.
DR InterPro: IPR001650; Helicase_C.
DR Pfam: PF00270; DEAD_1.
DR Pfam: PF00271; Helicase_C_1.
DR SMART: SM00487; DEXDC_1.
DR SMART: SM00490; HELIC_C_1.
DR PROSITE: PS00039; DEAD_ATP_HELICASE; 1.
KW ATP-binding; Helicase; RNA-binding.
FT NP BIND 113 120 ATP (Potential).
FT SITE 222 225 DEAD box.
FT CONFLICT 647 647 A -> D (in Ref. 2).
FT CONFLICT 658 658 D -> E (in Ref. 2).
FT CONFLICT 661 661 N -> K (in Ref. 2).
SQ SEQUENCE 875 AA; 100815 MW; 4692DDA56AD945B5 CRC64;

Query Match 59.7%; Score 40; DB 1; Length 875;
Best Local Similarity 54.5%; Pred. No. 4,9e+02;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0.

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OY 1 EFGAGLVLGGQ 11
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Db 169 DFGAGLITGCK 179

Db 169 DFGAGLITGCK 195
| | | | |

Search completed: December 9, 2004, 09:20:51
Job time : 9.96223 secs

RESULT 40

080Y44 PRELIMINARY; PRT; 891 AA.
ID 080Y44
AC 080Y44; 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, last annotation update)
DE Ddx10 protein (Fragment).
CN Name=Ddx10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Utsdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalón D.K., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Fahney U., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RA Strausberg R.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the DEAD box helicase family.
DR EMBL; BC049261; AH49261.1; -.
DR MGD; MGI:1924841; Ddx10.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0008026; F:ATP-dependent helicase activity; IEA.
DR GO; GO:0016787; F:hydrolyase activity; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR001410; DEAD.
DR InterPro; IPR01545; DEAD/DEAH_N.
DR InterPro; IPR000629; DEAD_box.
DR InterPro; IPR001650; Helicase_C.
DR Pfam; PF00270; DEAD; 1.
DR Pfam; PF00271; Helicase_C; 1.
DR SMART; SM00487; DEXDC; 1.
DR SMART; SM00490; HELIC; 1.
DR PROSITE; PS00039; DEAD_ATP_HELICASE; 1.
KW ATP-binding; Helicase; Hydrolyase.
KW NON_TER 1
SQ SEQUENCE 891 AA; 102289 MW; FCCABBEFA9FA5892 CRC64;

Query Match 59.7%; Score 40; DB 2; Length 891;
Best Local Similarity 54.5%; Freq. No. 5e+02;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
OY 1 EFGAGLVLGGQ 11

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 9, 2004, 08:56:57 ; Search time 1.28597 Seconds
(without alignments)
670.415 Million cell updates/sec

Title: US-09-462-416-1
Perfect score: 67
Sequence: 1 EFGAGLVGQGF 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: Issued Patents AA: *
2: /cgn2_6/prodata/1/1aa/5A_COMB.pep: *
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4: /cgn2_6/prodata/1/1aa/5A_COMB.pep: *
5: /cgn2_6/prodata/1/1aa/6B_COMB.pep: *
6: /cgn2_6/prodata/1/1aa/6C_COMB.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Match	Length	DB	ID	Description
1	67	100.0	21	3	US-09-215-212-12	Sequence 12, Appl
2	67	100.0	34	3	US-09-215-212-13	Sequence 13, Appl
3	42	62.7	360	4	US-09-252-991A-18909	Sequence 18909, A
4	41	61.2	640	4	US-09-252-991A-27542	Sequence 27542, A
5	40	59.7	171	4	US-09-252-991A-32724	Sequence 32724, A
6	40	59.7	321	4	US-09-270-767-46190	Sequence 46190, A
7	38.5	57.5	903	4	US-09-252-991A-24977	Sequence 24977, A
8	38	56.7	494	4	US-09-252-991A-23386	Sequence 23386, A
9	37	55.2	149	4	US-09-270-767-33609	Sequence 33609, A
10	37	55.2	150	4	US-09-543-681A-7178	Sequence 7178, Ap
11	37	55.2	443	4	US-09-489-039A-11069	Sequence 11069, A
12	37	55.2	452	4	US-09-252-991A-31196	Sequence 31196, A
13	37	55.2	574	4	US-09-252-991A-33065	Sequence 33065, A
14	36.5	54.5	153	4	US-09-540-236-2968	Sequence 2968, Ap
15	36	53.7	239	4	US-09-252-991A-29929	Sequence 29929, A
16	36	53.7	239	4	US-09-252-991A-20850	Sequence 20850, A
17	36	53.7	242	4	US-09-134-000C-4497	Sequence 4497, Ap
18	36	53.7	278	4	US-09-252-991A-26774	Sequence 26774, A
19	36	53.7	473	4	US-09-252-991A-19484	Sequence 19484, A
20	36	53.7	584	4	US-08-845-295A-2	Sequence 2, Appl
21	36	53.7	584	3	US-09-140-933-2	Sequence 2, Appl
22	36	53.7	584	3	US-09-146-661-2	Sequence 2, Appl
23	36	53.7	584	3	US-09-150-515-2	Sequence 2, Appl
24	36	53.7	809	4	US-09-248-796A-19668	Sequence 19668, A
25	35	52.2	70	4	US-09-134-000C-6657	Sequence 6657, Ap
26	35	52.2	91	4	US-09-134-000C-5500	Sequence 5500, Ap
27	35	52.2	97	4	US-09-248-796A-21582	Sequence 21582, A

28	35	52.2	107	4	US-09-621-976-5202	Sequence 5202, Ap
29	35	52.2	120	3	US-09-107-858-22	Sequence 22, Appl
30	35	52.2	120	3	US-09-107-858-23	Sequence 23, Appl
31	35	52.2	120	4	US-09-579-174-22	Sequence 22, Appl
32	35	52.2	120	4	US-09-579-174-23	Sequence 23, Appl
33	35	52.2	196	3	US-09-247-155-163	Sequence 163, Appl
34	35	52.2	222	1	US-07-732-242C-7	Sequence 7, Appl
35	35	52.2	229	4	US-10-140-002-472	Sequence 472, Appl
36	35	52.2	252	3	US-08-513-974B-52	Sequence 52, Appl
37	35	52.2	252	3	US-08-513-974B-360	Sequence 360, Appl
38	35	52.2	252	4	US-09-461-436B-52	Sequence 52, Appl
39	35	52.2	339	2	US-08-758-621-2	Sequence 2, Appl
40	35	52.2	339	3	US-09-107-858-2	Sequence 2, Appl
41	35	52.2	339	4	US-09-579-174-2	Sequence 2, Appl
42	35	52.2	345	2	US-08-758-621-14	Sequence 14, Appl
43	35	52.2	345	3	US-09-107-858-14	Sequence 14, Appl
44	35	52.2	345	4	US-09-579-174-14	Sequence 14, Appl
45	35	52.2	434	4	US-09-252-991A-27456	Sequence 27456, A

ALIGNMENTS

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RESULT 1
US-09-215-212-12
; Sequence 12, Application US/09215212
; Patent No. 6372207
; GENERAL INFORMATION:
; APPLICANT: TEPPER, Mark
; APPLICANT: CUNNINGHAM, Mark
; APPLICANT: SHERRIS, David
; APPLICANT: EL TAYAR, Nabil
; APPLICANT: MCKENNA, Sean
; TITLE OF INVENTION: IFNAR2/IFN COMPLEX
; FILE REFERENCE: TEPPER/IA.SEQ
; CURRENT APPLICATION NUMBER: US/09/215, 212
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 60/068, 295
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 12
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: C terminal human
US-09-215-212-12
;
Query Match      100.0%   Score 67;   DB 3;   Length 21;
Best Local Similarity 100.0%;   Pred. No. 0.00023;
Matches 13;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

Oy      1 EFGAGLVGQGF 13
Db      6 EFGAGLVGQGF 18

RESULT 2
US-09-215-212-13
; Sequence 13, Application US/09215212
; Patent No. 6372207
; GENERAL INFORMATION:
; APPLICANT: TEPPER, Mark
; APPLICANT: CUNNINGHAM, Mark
; APPLICANT: SHERRIS, David
; APPLICANT: EL TAYAR, Nabil
; APPLICANT: MCKENNA, Sean
; TITLE OF INVENTION: IFNAR2/IFN COMPLEX
; FILE REFERENCE: TEPPER/IA.SEQ
; CURRENT APPLICATION NUMBER: US/09/215, 212
; CURRENT FILING DATE: 1998-12-18

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;; PRIOR APPLICATION NUMBER: 60/068,295
;; PRIOR FILING DATE: 1997-12-19
;; NUMBER OF SEQ ID NOS: 15
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 13
;; LENGTH: 34
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: C terminal human
;; OTHER INFORMATION: sIFMAR2 linked by linker to N terminal human IFNbeta
US-09-215-212-13

Query Match 100.0%; Score 67; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.00038;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EFGAGLVGGQFM 13
Db 6 EFGAGLVGGQFM 18

RESULT 3
US-09-252-991A-18909
;; Sequence 18909, Application US/09252991A
;; Patent No. 6551795
;; GENERAL INFORMATION:
;; APPLICANT: Marc J. Rubenfield et al.
;; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;; FILE REFERENCE: 107196.136
;; CURRENT APPLICATION NUMBER: US/09/252,991A
;; CURRENT FILING DATE: 1999-02-18
;; PRIOR APPLICATION NUMBER: US 60/074,788
;; PRIOR FILING DATE: 1998-02-18
;; PRIOR APPLICATION NUMBER: US 60/094,190
;; PRIOR FILING DATE: 1998-07-27
;; NUMBER OF SEQ ID NOS: 33142
;; SEQ ID NO 18909
;; LENGTH: 360
;; TYPE: PRT
;; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18909

Query Match 62.7%; Score 42; DB 4; Length 360;
Best Local Similarity 80.0%; Pred. No. 42;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GAGLVGGQF 12
Db 202 GAGLVGGQF 211

RESULT 4
US-09-252-991A-27542
;; Sequence 27542, Application US/09252991A
;; Patent No. 6551795
;; GENERAL INFORMATION:
;; APPLICANT: Marc J. Rubenfield et al.
;; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;; FILE REFERENCE: 107196.136
;; CURRENT APPLICATION NUMBER: US/09/252,991A
;; CURRENT FILING DATE: 1999-02-18
;; PRIOR APPLICATION NUMBER: US 60/074,788
;; PRIOR FILING DATE: 1998-02-18
;; PRIOR APPLICATION NUMBER: US 60/094,190
;; PRIOR FILING DATE: 1998-07-27
;; NUMBER OF SEQ ID NOS: 33142
;; SEQ ID NO 27542
;; LENGTH: 640
;; TYPE: PRT
;; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-27542

Query Match 61.2%; Score 41; DB 4; Length 640;
Best Local Similarity 80.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 FGAGLVGGQ 11
Db 304 FGAGLVGGQ 313

RESULT 5
US-09-252-991A-32724
;; Sequence 32724, Application US/09252991A
;; Patent No. 6551795
;; GENERAL INFORMATION:
;; APPLICANT: Marc J. Rubenfield et al.
;; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;; FILE REFERENCE: 107196.136
;; CURRENT APPLICATION NUMBER: US/09/252,991A
;; CURRENT FILING DATE: 1999-02-18
;; PRIOR APPLICATION NUMBER: US 60/074,788
;; PRIOR FILING DATE: 1998-02-18
;; PRIOR APPLICATION NUMBER: US 60/094,190
;; PRIOR FILING DATE: 1998-07-27
;; NUMBER OF SEQ ID NOS: 33142
;; SEQ ID NO 32724
;; LENGTH: 171
;; TYPE: PRT
;; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-32724

Query Match 59.7%; Score 40; DB 4; Length 171;
Best Local Similarity 77.8%; Pred. No. 40;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FGAGLVGG 10
Db 101 FGAGLVGG 109

RESULT 6
US-09-270-767-46190
;; Sequence 46190, Application US/09270767
;; Patent No. 6703491
;; GENERAL INFORMATION:
;; APPLICANT: Homburger et al.
;; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
;; FILE REFERENCE: File Reference: 7326-094
;; CURRENT APPLICATION NUMBER: US/09/270,767
;; CURRENT FILING DATE: 1999-03-17
;; NUMBER OF SEQ ID NOS: 62517
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 46190
;; LENGTH: 321
;; TYPE: PRT
;; ORGANISM: Drosophila melanogaster
;; FEATURE:
;; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-46190

Query Match 59.7%; Score 40; DB 4; Length 321;
Best Local Similarity 54.5%; Pred. No. 77;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EFGAGLVGGQ 11
Db 189 DFSAGLVGGQ 199

RESULT 7
US-09-252-991A-24977


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Sequence 24977, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 24977
; LENGTH: 503
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24977

Query Match
Best Local Similarity 57.5%; Score 38.5; DB 4; Length 903;
Matches 9; Conservative 1; Mismatches 1; Gaps 1; Indels 3;

OY 2 FGAG--LVLGGGF 12
DB 509 FGAGPALALGGGF 522

RESULT 8
US-09-252-991A-23386
; Sequence 23386, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23386
; LENGTH: 494
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23386

Query Match
Best Local Similarity 56.7%; Score 38; DB 4; Length 494;
Matches 7; Conservative 1; Mismatches 1; Gaps 0; Indels 0;

OY 3 GAGLVGGQ 11
DB 398 GGGLVGGG 406

RESULT 9
US-09-270-767-33609
; Sequence 33609, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; PRIOR FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33609
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; LENGTH: 149
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-33609

Query Match
Best Local Similarity 55.2%; Score 37; DB 4; Length 149;
Matches 6; Conservative 2; Mismatches 2; Gaps 0; Indels 0;

OY 3 GAGLVGGQ 12
DB 94 GGGLVGGQ 103

RESULT 10
US-09-543-681A-7178
; Sequence 7178, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 7178
; LENGTH: 150
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-7178

Query Match
Best Local Similarity 55.2%; Score 37; DB 4; Length 150;
Matches 6; Conservative 2; Mismatches 1; Gaps 0; Indels 0;

OY 2 FGAGLVGG 10
DB 26 FSAGLVGG 34

RESULT 11
US-09-489-039A-11069
; Sequence 11069, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 11069
; LENGTH: 443
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11069

Query Match
Best Local Similarity 55.2%; Score 37; DB 4; Length 443;
Matches 7; Conservative 2; Mismatches 2; Gaps 0; Indels 0;

OY 2 FGAGLVGGGF 12
DB 136 FGGLVGGGW 146

RESULT 12
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US-09-252-991A-31196
; Sequence 31196, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 31196
; LENGTH: 452
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31196

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Query Match
Best Local Similarity 55.2%; Score 37; DB 4; Length 452;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

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QY 1 EFGAGLVGGGFM 13
DB 288 EFGAGLVGGGFM 300

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RESULT 13
US-09-252-991A-33065
; Sequence 33065, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 33065
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-33065

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```

Query Match
Best Local Similarity 55.2%; Score 37; DB 4; Length 574;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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```

QY 2 FGAAGLVGGGFM 12
DB 136 FGAAGLVGGGFM 146

```

```

RESULT 14
US-09-540-236-2968
; Sequence 2968, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; PRIOR FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840

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; SEQ ID NO 2968
; LENGTH: 153
; TYPE: PRT
; ORGANISM: M.catarrhalis
US-09-540-236-2968

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Query Match
Best Local Similarity 54.5%; Score 36.5; DB 4; Length 153;
Matches 7; Conservative 4; Mismatches 1; Indels 3; Gaps 1;

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QY 2 FGAAGLVGGGFM 13
DB 21 FGAAGLVGGGFM 35

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RESULT 15
US-09-252-991A-29929
; Sequence 29929, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 29929
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29929

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Query Match
Best Local Similarity 53.7%; Score 36; DB 4; Length 213;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 3 GAGLVGGG 10
DB 143 GAGLVGGG 150

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```

RESULT 16
US-09-252-991A-20850
; Sequence 20850, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 20850
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20850

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Query Match
Best Local Similarity 53.7%; Score 36; DB 4; Length 239;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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```

QY 1 EFGAGLVGGG 10

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Db 162 ELGAGVYAGG 171

RESULT 17
US-09-134-000C-4497

Sequence 4497, Application US/09134000C

Patent No. 6617155

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 032796-032

CURRENT APPLICATION NUMBER: US/09/134,000C

CURRENT FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/055,778

PRIOR FILING DATE: 1997-08-15

NUMBER OF SEQ ID NOS: 6812

SOFTWARE: Patentin version 3.1

SEQ ID NO 4497

LENGTH: 242

TYPE: PRT

ORGANISM: Enterococcus faecalis

US-09-134-000C-4497

Query Match 53.7%; Score 36; DB 4; Length 242;
Best Local Similarity 87.5%; Pred. No. 2.5e+02;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EFGAGLV 8
Db 45 EFGAGLV 52

RESULT 18

US-09-252-991A-26774

Sequence 26774, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 26774

LENGTH: 278

TYPE: PRT

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-26774

Query Match 53.7%; Score 36; DB 4; Length 278;
Best Local Similarity 63.6%; Pred. No. 2.3e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 FGAGLVGGGF 12
Db 158 FGAGLVGGGF 168

RESULT 19

US-09-252-991A-19484

Sequence 19484, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 19484

LENGTH: 473

TYPE: PRT

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-19484

Query Match 53.7%; Score 36; DB 4; Length 473;
Best Local Similarity 77.8%; Pred. No. 5e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 AGLVGGGF 12
Db 109 AGLVGGGF 117

RESULT 20

US-08-845-295A-2

Sequence 2, Application US/08845295A

Patent No. 5817490

GENERAL INFORMATION:

APPLICANT: Hubbs, John C.

TITLE OF INVENTION: Enzymatic Process for the Manufacture of

TITLE OF INVENTION: Ascorbic Acid, 2-Keto-L-Gulonic Acid, and Esters of

TITLE OF INVENTION: 2-Keto-L-Gulonic Acid

NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:

ADDRESSEE: Eastman Chemical Company

STREET: P.O. Box 511

CITY: Kingsport

STATE: Tennessee

COUNTRY: USA

ZIP: 37662-5075

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch disk

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows 95

SOFTWARE: Microsoft Word

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/845,295A

FILING DATE: 25-April-97

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/017,879

FILING DATE: 17-MAY-1996

ATTORNEY/AGENT INFORMATION:

NAME: Cheryl J. Tubach

REGISTRATION NUMBER: 38,346

TELEPHONE: 423-229-1239

TELEFAX: 423-229-1239

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 584 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

MOLECULE TYPE: protein

US-08-845-295A-2

Query Match 53.7%; Score 36; DB 2; Length 584;
Best Local Similarity 87.5%; Pred. No. 6.3e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GAGLVGG 10
Db 1 GAGLVGG 10

Db 146 GGGVLGG 153

RESULT 21

US-09-140-933-2

Sequence 2, Application US/09140933

Patent No. 6022719

GENERAL INFORMATION:

APPLICANT: Hubbs, John C.

TITLE OF INVENTION: Enzymatic Process for the Manufacture of

TITLE OF INVENTION: Ascorbic Acid, 2-Keto-L-Gulonic Acid, and Esters of

NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESSES:

ADDRESSER: Eastman Chemical Company

STREET: P.O. Box 511

CITY: Kingsport

STATE: Tennessee

COUNTRY: USA

ZIP: 37662-5075

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch disk

OPERATING SYSTEM: Windows 95

SOFTWARE: Microsoft Word

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/140,933

FILING DATE: 27-August-98

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/017,879; 08/845,295

FILING DATE: 17-May-96; 25-April-97

ATTORNEY/AGENT INFORMATION:

NAME: Cheryl J. Tubach

REGISTRATION NUMBER: 38,346

REFERENCE/DOCKET NUMBER: 70432

TELEPHONE: 423-229-6189

TELEFAX: 423-229-1239

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 584 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

MOLECULE TYPE: protein

US-09-140-933-2

Query Match 53.7%; Score 36; DB 3; Length 584;
Best Local Similarity 87.5%; Pred. No. 6.3e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GAGVLGG 10
Db 146 GGGVLGG 153

RESULT 22

US-09-146-661-2

Sequence 2, Application US/09146661

Patent No. 6136575

GENERAL INFORMATION:

APPLICANT: Hubbs, John C.

TITLE OF INVENTION: Enzymatic Process for the Manufacture of

TITLE OF INVENTION: Ascorbic Acid, 2-Keto-L-Gulonic Acid, and Esters of 2-Keto-L-Gu-

NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESSES:

ADDRESSER: Eastman Chemical Company

STREET: P.O. Box 511

CITY: Kingsport

STATE: Tennessee

COUNTRY: USA

ZIP: 37662-5075

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk
OPERATING SYSTEM: Windows 95
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/150,515
FILING DATE: 09-SEP-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/017,879; 08/845,295
FILING DATE: 17-May-96; 25-April-97
ATTORNEY/AGENT INFORMATION:
NAME: Cheryl J. Tubach
REGISTRATION NUMBER: 38,346
REFERENCE/DOCKET NUMBER: 70432
TELEPHONE: 423-229-6189
TELEFAX: 423-229-1239
INFORMATION FOR SEQ ID NO: 2:

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch disk

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows 95

SOFTWARE: Microsoft Word

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/146,661

FILING DATE: 03-September-98

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/017,879; 08/845,295

FILING DATE: 17-May-96; 25-April-97

ATTORNEY/AGENT INFORMATION:

NAME: Cheryl J. Tubach

REGISTRATION NUMBER: 38,346

REFERENCE/DOCKET NUMBER: 70432

TELEPHONE: 423-229-6189

TELEFAX: 423-229-1239

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 584 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

MOLECULE TYPE: protein

US-09-146-661-2

Query Match 53.7%; Score 36; DB 3; Length 584;
Best Local Similarity 87.5%; Pred. No. 6.3e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GAGVLGG 10
Db 146 GGGVLGG 153

RESULT 23

US-09-150-515-2

Sequence 2, Application US/09150515

Patent No. 6271006

GENERAL INFORMATION:

APPLICANT: Hubbs, John C.

TITLE OF INVENTION: Enzymatic Process for the Manufacture of

TITLE OF INVENTION: Ascorbic Acid, 2-Keto-L-Gulonic Acid, and Esters of

NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESSES:

ADDRESSER: Eastman Chemical Company

STREET: P.O. Box 511

CITY: Kingsport

STATE: Tennessee

COUNTRY: USA

ZIP: 37662-5075

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch disk

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows 95

SOFTWARE: Microsoft Word

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/150,515

FILING DATE: 09-SEP-1998

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/017,879; 08/845,295

FILING DATE: 17-May-96; 25-April-97

ATTORNEY/AGENT INFORMATION:

NAME: Cheryl J. Tubach

REGISTRATION NUMBER: 38,346

REFERENCE/DOCKET NUMBER: 70432

TELEPHONE: 423-229-6189

TELEFAX: 423-229-1239

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
LENGTH: 584 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
MOLECULE TYPE: protein
US-09-150-515-2

Query Match 53.7%; Score 36; DB 3; Length 584;
Best Local Similarity 87.5%; Pred. No. 6.3e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GAGLVVGG 10
DB 146 GGGVLVGG 153

RESULT 24
US-09-248-796A-19668
; Sequence 19668, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 19668
; LENGTH: 809
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-19668

Query Match 53.7%; Score 36; DB 4; Length 809;
Best Local Similarity 70.0%; Pred. No. 8.8e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 FGAGLVGGQ 11
DB 193 FSGLVGTGCK 202

RESULT 25
US-09-134-000C-6657
; Sequence 6657, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6657
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-6657

Query Match 52.2%; Score 35; DB 4; Length 70;
Best Local Similarity 66.7%; Pred. No. 97;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 FGAGLVGG 10

DB 31 FGLGLVGG 39

RESULT 26
US-09-134-000C-5500
; Sequence 5500, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5500
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-5500

Query Match 52.2%; Score 35; DB 4; Length 91;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 FGAGLVGG 10
DB 49 FGLGLVGG 57

RESULT 27
US-09-248-796A-21582
; Sequence 21582, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 21582
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-21582

Query Match 52.2%; Score 35; DB 4; Length 97;
Best Local Similarity 50.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EFGAGLVGGQF 12
DB 48 KFGTKLINGEF 59

RESULT 28
US-09-621-976-5202
; Sequence 5202, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.

```

; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 5202
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -23..-1
US-09-621-976-5202

Query Match
Best Local Similarity 52.2%; Score 35; DB 4; Length 107;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 FGAGLVGGQFM 13
Db 80 GLGLLGGGLM 90

RESULT 29
US-09-107-858-22
; Sequence 22, Application US/09107858
; Patent No. 6162900
; GENERAL INFORMATION:
; APPLICANT: Guerinet, Mary Lou et al.
; TITLE OF INVENTION: METAL-REGULATED TRANSPORTERS AND USES THEREFOR
; FILE REFERENCE: DCI-099CPDV
; CURRENT APPLICATION NUMBER: US/09/107,858
; CURRENT FILING DATE: 1998-06-30
; EARLIER APPLICATION NUMBER: 08/758,621
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 22
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-107-858-22

Query Match
Best Local Similarity 52.2%; Score 35; DB 3; Length 120;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 FGAGLVGGQFM 13
Db 77 FASGIIIGTGFM 88

RESULT 30
US-09-107-858-23
; Sequence 23, Application US/09107858
; Patent No. 6162900
; GENERAL INFORMATION:
; APPLICANT: Guerinet, Mary Lou et al.
; TITLE OF INVENTION: METAL-REGULATED TRANSPORTERS AND USES THEREFOR
; FILE REFERENCE: DCI-099CPDV
; CURRENT APPLICATION NUMBER: US/09/107,858
; CURRENT FILING DATE: 1998-06-30
; EARLIER APPLICATION NUMBER: 08/758,621
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 23
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-107-858-23
```

```

Query Match
Best Local Similarity 52.2%; Score 35; DB 3; Length 120;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 FGAGLVGGQFM 13
Db 77 FSSGIIIGTGFM 88

RESULT 31
US-09-579-174-22
; Sequence 22, Application US/09579174
; Patent No. 6590140
; GENERAL INFORMATION:
; APPLICANT: Guerinet, Mary Lou et al.
; TITLE OF INVENTION: METAL-REGULATED TRANSPORTERS AND USES THEREFOR
; FILE REFERENCE: DCI-099CPDV
; CURRENT APPLICATION NUMBER: US/09/579,174
; CURRENT FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 09/107,858
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: 08/758,621
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 22
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-579-174-22

Query Match
Best Local Similarity 52.2%; Score 35; DB 4; Length 120;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 FGAGLVGGQFM 13
Db 77 FASGIIIGTGFM 88

RESULT 32
US-09-579-174-23
; Sequence 23, Application US/09579174
; Patent No. 6590140
; GENERAL INFORMATION:
; APPLICANT: Guerinet, Mary Lou et al.
; TITLE OF INVENTION: METAL-REGULATED TRANSPORTERS AND USES THEREFOR
; FILE REFERENCE: DCI-099CPDV
; CURRENT APPLICATION NUMBER: US/09/579,174
; CURRENT FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 09/107,858
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: 08/758,621
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 23
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-579-174-23

Query Match
Best Local Similarity 52.2%; Score 35; DB 4; Length 120;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 FGAGLVGGQFM 13
Db 77 FSSGIIIGTGFM 88

RESULT 33
US-09-247-155-163
```

```

; Sequence 163, Application US/09247155A
; Patent No. 6312922
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bouguet, Lydie
; TITLE OF INVENTION: Complementary DNAs
; FILE REFERENCE: GENSET 021A
; CURRENT APPLICATION NUMBER: US/09/247,155A
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/074,121
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/081,563
; EARLIER FILING DATE: 1998-04-13
; EARLIER APPLICATION NUMBER: 60/096,116
; EARLIER FILING DATE: 1998-08-10
; EARLIER APPLICATION NUMBER: 60/099,273
; EARLIER FILING DATE: 1998-10-04
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: Patent.pm
; SEQ ID NO 163
; LENGTH: 196
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -34..-1
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 81,84,87,131,135,143,156
; OTHER INFORMATION: Xaa = any one of the twenty amino acids
; US-09-247-155-163

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```

Query Match      52.2%; Score 35; DB 3; Length 196;
Best Local Similarity 54.5%; Pred. No. 2.9e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```

```

QY      3 GAGLVGGGPM 13
DB      176 GAGFIIIGGIV 186

```

```

RESULT 34
US-07-732-242C-7
; Sequence 7, Application US/07732242C
; Patent No. 5296399
; GENERAL INFORMATION:
; APPLICANT: Uozumi, Takeshi; Masaki, Haruhiko;
; APPLICANT: Hidaka, Makoto; Nakamura, Akira;
; APPLICANT: Maeda, Michihisa; Yoneta, Yasuo
; TITLE OF INVENTION: Gene of Urease
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Frieauff, Holtz, Goodman & Woodward, P.C.
; STREET: 600 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10016-2088
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 0.72mb
; COMPUTER: IBM PC compatible (NEC PC-9801 RX)
; OPERATING SYSTEM: MS DOS
; SOFTWARE: ASCII Form
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/732,242C
; FILING DATE: 19910718
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JPN 2-210178
; FILING DATE: 10-AUG-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Goodman, Herbert

```

```

; REGISTRATION NUMBER: 17081
; REFERENCE/DOCKET NUMBER: 910532/HG
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)972-1400
; TELEFAX: (212)370-1622
; TELEX: 236268
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 222 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-07-732-242C-7

```

```

Query Match      52.2%; Score 35; DB 1; Length 222;
Best Local Similarity 87.5%; Pred. No. 3.3e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      2 FGAGLVG 9
DB      164 FGAGTVLG 171

```

```

RESULT 35
US-10-140-002-472
; Sequence 472, Application US/10140002
; Patent No. 6725730
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Geriltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C59
; CURRENT APPLICATION NUMBER: US/10/140,002
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 472
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-140-002-472

```

```

Query Match      52.2%; Score 35; DB 4; Length 229;
Best Local Similarity 54.5%; Pred. No. 3.4e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```

```

QY      3 GAGLVGGGPM 13
DB      176 GAGFIIIGGIV 186

```

```

RESULT 36
US-08-513-974B-52
; Sequence 52, Application US/08513974B
; Patent No. 6114139
; GENERAL INFORMATION:

```

APPLICANT: Hinuma, Shuji
APPLICANT: Hosoya, Masaki
APPLICANT: Fujii, Ryo
APPLICANT: Ohtaki, Tetsuya
APPLICANT: Fukusumi, Shoji
APPLICANT: Ohgi, Kazuhiro
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
NUMBER OF SEQUENCES: 380
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/513,974B
FILING DATE: 14-SEP-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/01599
FILING DATE: 10-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-093989
FILING DATE: 19-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-057186
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-007177
FILING DATE: 20-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-326611
FILING DATE: 28-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-270017
FILING DATE: 02-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236357
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236356
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189274
FILING DATE: 11-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189273
FILING DATE: 11-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189272
FILING DATE: 11-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Resnick, David S.
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 45753
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 252 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-513-974B-52

Query Match 52.2%; Score 35; DB 3; Length 252;
Best Local Similarity 44.4%; Pred. No. 3.7e+02;
Matches 8; Conservative 2; Mismatches 2; Indels 6; Gaps 1;
Qy 2 FGAG-----LVVGQPM 13
Db 196 FGGAIVLLAVGGQFL 213
RESULT 37
US-08-513-974B-360
Sequence 360, Application US/08513974B
Patent No. 614139
GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
APPLICANT: Hosoya, Masaki
APPLICANT: Fujii, Ryo
APPLICANT: Ohtaki, Tetsuya
APPLICANT: Fukusumi, Shoji
APPLICANT: Ohgi, Kazuhiro
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
NUMBER OF SEQUENCES: 380
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/513,974B
FILING DATE: 14-SEP-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/01599
FILING DATE: 10-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-093989
FILING DATE: 19-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-057186
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-007177
FILING DATE: 20-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-326611
FILING DATE: 28-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-270017
FILING DATE: 02-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236357
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236356
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189274
FILING DATE: 11-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189273
FILING DATE: 11-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189272
FILING DATE: 11-AUG-1994

ATTORNEY/AGENT INFORMATION:
NAME: Resnick, David S.
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 45753
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 360:
SEQUENCE CHARACTERISTICS:
LENGTH: 252 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-513-974B-360

Query Match 52.2%; Score 35; DB 3; Length 252;
Best Local Similarity 44.4%; Pred. No. 3.7e+02;
Matches 8; Conservative 2; Mismatches 2; Indels 6; Gaps 1;

QY 2 FGAG-----LVYGGQFM 13
DB 196 FGAGKAUVLAVGGQFL 213

RESULT 38
US-09-461-436B-52
Sequence 52, Application US/09461436B
Patent No. 6538107
GENERAL INFORMATION:
APPLICANT: Shuji Hinuma
Yasunaki Ito
Ryo Fujii
TITLE OF INVENTION: G Protein Coupled Receptor Protein,
Production, And Use Thereof
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Edwards & Angel, LLP
STREET: 101 Federal Street
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02209
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/461,436B
FILING DATE: 14-Dec-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/513,974
FILING DATE: 14-SEP-1995
APPLICATION NUMBER: PCT/JP95/01599
FILING DATE: 10-AUG-1995
APPLICATION NUMBER: 7-093989
FILING DATE: 19-APR-1995
APPLICATION NUMBER: 7-057186
FILING DATE: 16-MAR-1995
APPLICATION NUMBER: 7-007177
FILING DATE: 20-JAN-1995
APPLICATION NUMBER: 6-326611
FILING DATE: 28-DEC-1994
APPLICATION NUMBER: 6-270017
FILING DATE: 02-NOV-1994
APPLICATION NUMBER: 6-236357
FILING DATE: 30-SEP-1994
APPLICATION NUMBER: 6-236356
FILING DATE: 30-SEP-1994
APPLICATION NUMBER: 6-189274
FILING DATE: 11-AUG-1994
APPLICATION NUMBER: 6-189273

FILING DATE: 11-AUG-1994
APPLICATION NUMBER: 6-189272
FILING DATE: 11-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: CONLIN, DAVID G.
REGISTRATION NUMBER: <Unknown>
REFERENCE/DOCKET NUMBER: 45753 DIV2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-439-4444
TELEFAX: 617-439-4170
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 252 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 52:
US-09-461-436B-52

Query Match 52.2%; Score 35; DB 4; Length 252;
Best Local Similarity 44.4%; Pred. No. 3.7e+02;
Matches 8; Conservative 2; Mismatches 2; Indels 6; Gaps 1;

QY 2 FGAG-----LVYGGQFM 13
DB 196 FGAGKAUVLAVGGQFL 213

RESULT 39
US-08-758-621-2
Sequence 52, Application US/08758621
Patent No. 5846821
GENERAL INFORMATION:
APPLICANT: Gueriot, Mary Lou, and Eide, David J.
TITLE OF INVENTION: Metal-Regulated Transporters and Uses Therefor
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/758,621
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/018,578
FILING DATE: 29-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Silveri, Jean W.
REGISTRATION NUMBER: 39,030
REFERENCE/DOCKET NUMBER: DCI-099CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-758-621-2

Query Match 52.2%; Score 35; DB 2; Length 339;
Best Local Similarity 50.0%; Pred. No. 5.1e+02;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 FGAGLVIGQFM 13
 Db 84 FASGIILGTGFM 95

RESULT 40
 US-09-107-858-2
 ; Sequence 2, Application US/09107858
 ; Patent No. 6162900
 ; GENERAL INFORMATION:
 ; APPLICANT: Guerinet, Mary Lou et al.
 ; TITLE OF INVENTION: METAL-REGULATED TRANSPORTERS AND USES THEREFOR
 ; FILE REFERENCE: DCI-099CPDV
 ; CURRENT APPLICATION NUMBER: US/09/107,858
 ; CURRENT FILING DATE: 1998-06-30
 ; EARLIER APPLICATION NUMBER: 08/758,621
 ; EARLIER FILING DATE: 1996-11-27
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 339
 ; TYPE: PRT
 ; ORGANISM: Arabidopsis thaliana
 US-09-107-858-2

Query Match 52.2%; Score 35; DB 3; Length 339;
 Best Local Similarity 50.0%; Pred. No. 5.1e+02;
 Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 2 FGAGLVIGQFM 13
 Db 84 FASGIILGTGFM 95

Search completed: December 9, 2004, 09:22:45
 Job time : 2.28597 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 9, 2004, 08:56:57 ; Search time 53.714 Seconds
(without alignments)
670.415 Million cell updates/sec

Title: US-09-462-416-7

Perfect score: 2861

Sequence: 1 MVAVGCALLAALPAAGAL.....LILRSFKERLQSSLRALQW 543

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Issued Patents AA:*

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4: /cgn2_6/prodata/1/1aa/6B_COMB.pep:.*
5: /cgn2_6/prodata/1/1aa/PCTUS_COMB.pep:.*
6: /cgn2_6/prodata/1/1aa/Backfillseq1.pep:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1921	67.1	592	4	US-09-313-942-8
2	1918	67.0	468	3	US-08-795-473B-5
3	1918	67.0	468	4	US-09-439-856-5
4	1918	67.0	468	6	5171840-2
5	1918	67.0	468	6	5480796-2
6	1910	66.8	360	4	US-09-313-942-15
7	1852	64.7	344	6	5171840-7
8	1852	64.7	344	6	5480796-7
9	1788	62.5	1158	4	US-09-313-942-26
10	1783	62.3	1158	4	US-09-313-942-24
11	1741	60.9	323	6	5171840-6
12	1741	60.9	323	6	5480796-6
13	1683	58.8	315	4	US-09-313-942-16
14	1389	48.5	386	6	5171840-5
15	1389	48.5	386	6	5480796-5
16	1153	40.3	210	3	US-09-043-785-1
17	950	33.2	201	6	5171840-11
18	939	32.8	185	2	US-08-716-317-7
19	938.5	32.8	212	1	US-08-792-019B-9
20	938.5	32.8	212	3	US-08-988-819-9
21	938.5	32.8	212	3	US-09-016-534-9
22	938.5	32.8	212	3	US-08-097-869-7
23	938.5	32.8	212	3	US-08-795-473B-6
24	938.5	32.8	212	3	US-09-230-637-45
25	938.5	32.8	212	3	US-09-230-371A-27
26	938.5	32.8	212	4	US-09-439-856-6
27	938.5	32.8	212	4	US-09-462-941-13

28	938.5	32.8	212	6	5510472-2	Patent No. 5510472
29	935	32.7	317	3	US-08-469-318-145	Sequence 145, App
30	935	32.7	317	3	US-08-468-609A-145	Sequence 145, App
31	935	32.7	317	3	US-08-446-872A-145	Sequence 145, App
32	935	32.7	317	4	US-08-762-227A-145	Sequence 145, App
33	935	32.7	317	5	PCT-US95-01185-145	Sequence 2, Appl1
34	934	32.6	184	1	US-08-567-047-2	Sequence 2, Appl1
35	934	32.6	184	2	US-08-567-048-2	Sequence 2, Appl1
36	934	32.6	184	6	5186931-1	Patent No. 5186931
37	934	32.6	185	1	US-07-632-070B-1	Sequence 1, Appl1
38	934	32.6	185	1	US-07-918-181A-2	Sequence 2, Appl1
39	934	32.6	185	1	US-08-231-575-2	Sequence 2, Appl1
40	934	32.6	185	1	US-08-246-427A-5	Sequence 5, Appl1
41	934	32.6	185	2	US-08-766-620-5	Sequence 2, Appl1
42	934	32.6	185	5	PCT-US93-06928-2	Sequence 2, Appl1
43	934	32.6	185	6	5186931-2	Patent No. 5186931
44	934	32.6	186	1	US-07-632-070B-2	Sequence 2, Appl1
45	934	32.6	186	1	US-07-745-382-20	Sequence 20, Appl1

ALIGNMENTS

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RESULT 1
US-09-313-942-8
; Sequence 8, Application US/09313942
; Patent No. 6472179
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-A
; CURRENT APPLICATION NUMBER: US/09/313, 942
; PRIOR FILING DATE: 1999-05-19
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-313-942-8

Query Match      67.1%; Score 1921; DB 4; Length 592;
Best Local Similarity 77.1%; Pred. No. 86-151;
Matches 377; Conservative 22; Mismatches 44; Indels 46; Gaps 5;

QY      1 MVAVGCALLAALPAAGALARRCPADEVANGUTLSLPDGSVTLTCPCVPEEDNATYHW 60
DB      1 MVAVGCALLAALPAAGALARRCPADEVANGUTLSLPDGSVTLTCPCVPEEDNATYHW 60
QY      61 VLRKPAAGSHPRMAGMGRRLLRSVQLHDSGNYSCYRAGRAGTVAHLVDPPEEPOLS 120
DB      61 VLRKPAAGSHPRMAGMGRRLLRSVQLHDSGNYSCYRAGRAGTVAHLVDPPEEPOLS 120
QY      121 CERKSPLSNVCEWGRSTPSLTTRAVLLVRKFPNSPAEDFQEPQYSGESQKFSQCLAV 180
DB      121 CERKSPLSNVCEWGRSTPSLTTRAVLLVRKFPNSPAEDFQEPQYSGESQKFSQCLAV 180
QY      181 PGDGSFYTVSMCVASVSGSKFQOTPOGCILOPDPANITTVAVANPWLSTWQD 240
DB      181 PGDGSFYTVSMCVASVSGSKFQOTPOGCILOPDPANITTVAVANPWLSTWQD 240
QY      241 PHSNNSFYRLRFLRYRERSKFTTMMVKLOHHCIVHIDAMSGLRHVQVRAOEFPQ 300
DB      241 PHSNNSFYRLRFLRYRERSKFTTMMVKLOHHCIVHIDAMSGLRHVQVRAOEFPQ 300
QY      301 GEMSEWSPAMGTPTWESRSPPAENEVSTPMQALTTNKDDNIIIRDSANATSLPYEFMP 360
DB      301 GEMSEWSPAMGTPTWESRSPPAENEVSTPMQALTTNKDDNIIIRDSANATSLPYEFMP 360
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QY      361 VPFGEBSKVYAARHQPPLTSSERIDKQIRYLIDGISAARKETCNKSNMCE--SSKEALAE 418
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Db      358 -----PAGEP-----SCCKTHCPCCPAPELLGG 382
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QY      419 NNILNLPMAEKOCFCFSGFNEFTCLYKIIT--GLLEFVYLEYO--NRFESEEQAR 472
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Db      383 PSVFLEPPPKRDTLMTSRTEPVTCVVVDVSHEDPEVKNTMYDGVGHNAATKTREREQYN 442
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QY      473 AVQGSTKVL 481
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Db      443 STYRWVSVL 451
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RESULT 2
US-08-795-473B-5
: Sequence 5, Application US/08795473B
: Patent No. 6217858
: GENERAL INFORMATION:
: APPLICANT: Galun, Eithan
: APPLICANT: Nahot, Orit
: APPLICANT: Blum, Herbert E.
: TITLE OF INVENTION: A Pharmaceutical Composition for Treating
: TITLE OF INVENTION: Hepatitis B Virus (HBV) Infection
: NUMBER OF SEQUENCES: 10
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: Davidson, Davidson and Kappel, LLC
: STREET: 1140 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: USA
: ZIP: 10036
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: MS-DOS EDITOR
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/795,473B
: FILING DATE: 11-FEB-1997
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: Davidson, Clifford M.
: REGISTRATION NUMBER: 32,728
: REFERENCE/DOCKET NUMBER: 963,1007
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212)-997-1028
: TELEFAX: (212)-997-1037
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 468 amino acids
: TYPE: amino acid
: TOPOLOGY: unknown
US-08-795-473B-5

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Query Match 67.0%; Score 1918; DB 3; Length 468;

Matches 360; Conservative 1; Mismatches 4; Indels 8; Gaps 1;

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QY	VLTKPPAGSHPSFMAWGMGRLLILRSVOLHDSGNVSCYRAGRPMGYTHLLVDPVPEEPQLS	120
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QY	CFPKSPILSNVVCCEMGPSTPLTTKAILVLRKQNSPAEDFOEPCQYSQESQKFSCOLAV	180
Db	121 CFPKSPILSNVVCCEMGPSTPLTTKAILVLRKQNSPAEDFOEPCQYSQESQKFSCOLAV	180
QY	PGDSSFYIVSMCVASSVSGSKFSTQTFQCGGIIQDPDPNITVTVAANPRMLSVTWQD	240
Db	181 PGDSSFYIVSMCVASSVSGSKFSTQTFQCGGIIQDPDPNITVTVAANPRMLSVTWQD	240

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Db      181 PBGDSEFFIVSMCAVSSVGSKFKTQTFGGGIIQDPDPANIIYTAARBPMLSLVTWQD 240
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        |||||
Db      241 PHSWSSFFRLRFELRYAERSKFTTWMVDLOHCHVIDAMSGLNHVQLPAQEEFG 300
Qy      301 GEMSEMSPEAMGTPWTESSPPAENEVSTPMQALLTNKKDDNLLFRDSANATSLPYEFMP 360
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Db      301 GEMSEMSPEAMGTPWTESSPPAENEVSTPMQALLTNKKDDNLLFRDSANATSLPYEFMP 360
Qy      361 VPGEDSKDVAP 373
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Db      357 ----QDSSVPLP 365

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1  RESULT 3
2  US-09-439-856-5
3  ; Sequence 5, Application US/09439856
4  ; Patent No. 6410009
5  ; GENERAL INFORMATION:
6  ; APPLICANT: Galun, Eithan
7  ; APPLICANT: Nahot, Orit
8  ; APPLICANT: Blum, Herbert E.
9  ; TITLE OF INVENTION: A Pharmaceutical Composition for Treating
10 ; TITLE OF INVENTION: Hepatitis B Virus (HBV) Infection
11 ; NUMBER OF SEQUENCES: 10
12 ; CORRESPONDENCE ADDRESS:
13 ; ADDRESSEE: Davidson, Davidson and Kappel, LLC
14 ; STREET: 1140 Avenue of the Americas
15 ; CITY: New York
16 ; STATE: New York
17 ; COUNTRY: USA
18 ; ZIP: 10036
19 ; COMPUTER READABLE FORM:
20 ; MEDIUM TYPE: 3.5 inch disk
21 ; COMPUTER: IBM PC compatible
22 ; OPERATING SYSTEM: PC-DOS/MS-DOS
23 ; SOFTWARE: MS-DOS EDITOR
24 ; CURRENT APPLICATION DATA:
25 ; APPLICATION NUMBER: US/09/439,856
26 ; FILING DATE:
27 ; CLASSIFICATION:
28 ; PRIOR APPLICATION DATA:
29 ; APPLICATION NUMBER: 08/795,473
30 ; FILING DATE: 11-FEB-1997
31 ; ATTORNEY/AGENT INFORMATION:
32 ; NAME: Davidson, Clifford M.
33 ; REGISTRATION NUMBER: 32,728
34 ; REFERENCE/DOCKET NUMBER: 963,1007
35 ; TELECOMMUNICATION INFORMATION:
36 ; TELEPHONE: (212)-997-1028
37 ; TELEFAX: (212)-997-1037
38 ; INFORMATION FOR SEQ ID NO: 5:
39 ; SEQUENCE CHARACTERISTICS:
40 ; LENGTH: 468 amino acids
41 ; TYPE: amino acid
42 ; TOPOLOGY: unknown
43  US-09-439-856-5

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Query Match 67.0%; Score 1918; DB 4; Length 468;

Matches 360; Conservative 1; Mismatches 4; Indels 8; Gaps 1

QY	1	MAV	GAL	TA	ALL	AA	LP	AG	TA	LP	RR	CP	AG	SV	AG	VL	TL	SL	PG	ED	PN	TA	VM	60		
Db	1	MAV <td>GAL <td>TA <td>ALL <td>AA <td>LP <td>AG <td>TA <td>LP <td>RR <td>CP <td>AG <td>SV <td>AG <td>VL <td>TL <td>SL <td>PG <td>ED <td>PN <td>TA <td>VM <td>60</td> </td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td>	GAL <td>TA <td>ALL <td>AA <td>LP <td>AG <td>TA <td>LP <td>RR <td>CP <td>AG <td>SV <td>AG <td>VL <td>TL <td>SL <td>PG <td>ED <td>PN <td>TA <td>VM <td>60</td> </td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td>	TA <td>ALL <td>AA <td>LP <td>AG <td>TA <td>LP <td>RR <td>CP <td>AG <td>SV <td>AG <td>VL <td>TL <td>SL <td>PG <td>ED <td>PN <td>TA <td>VM <td>60</td> </td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td>	ALL <td>AA <td>LP <td>AG <td>TA <td>LP <td>RR <td>CP <td>AG <td>SV <td>AG <td>VL <td>TL <td>SL <td>PG <td>ED <td>PN <td>TA <td>VM <td>60</td> </td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td>	AA <td>LP <td>AG <td>TA <td>LP <td>RR <td>CP <td>AG <td>SV <td>AG <td>VL <td>TL <td>SL <td>PG <td>ED <td>PN <td>TA <td>VM <td>60</td> </td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td>	LP <td>AG <td>TA <td>LP <td>RR <td>CP <td>AG <td>SV <td>AG <td>VL <td>TL <td>SL <td>PG <td>ED <td>PN <td>TA <td>VM <td>60</td> </td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td>	AG <td>TA <td>LP <td>RR <td>CP <td>AG <td>SV <td>AG <td>VL <td>TL <td>SL <td>PG <td>ED <td>PN <td>TA <td>VM <td>60</td> </td></td></td></td></td></td></td></td></td></td></td></td></td></td></td>	TA <td>LP <td>RR <td>CP <td>AG <td>SV <td>AG <td>VL <td>TL <td>SL <td>PG <td>ED <td>PN <td>TA <td>VM <td>60</td> </td></td></td></td></td></td></td></td></td></td></td></td></td></td>	LP <td>RR <td>CP <td>AG <td>SV <td>AG <td>VL <td>TL <td>SL <td>PG <td>ED <td>PN <td>TA <td>VM <td>60</td> </td></td></td></td></td></td></td></td></td></td></td></td></td>	RR <td>CP <td>AG <td>SV <td>AG <td>VL <td>TL <td>SL <td>PG <td>ED <td>PN <td>TA <td>VM <td>60</td> </td></td></td></td></td></td></td></td></td></td></td></td>	CP <td>AG <td>SV <td>AG <td>VL <td>TL <td>SL <td>PG <td>ED <td>PN <td>TA <td>VM <td>60</td> </td></td></td></td></td></td></td></td></td></td></td>	AG <td>SV <td>AG <td>VL <td>TL <td>SL <td>PG <td>ED <td>PN <td>TA <td>VM <td>60</td> </td></td></td></td></td></td></td></td></td></td>	SV <td>AG <td>VL <td>TL <td>SL <td>PG <td>ED <td>PN <td>TA <td>VM <td>60</td> </td></td></td></td></td></td></td></td></td>	AG <td>VL <td>TL <td>SL <td>PG <td>ED <td>PN <td>TA <td>VM <td>60</td> </td></td></td></td></td></td></td></td>	VL <td>TL <td>SL <td>PG <td>ED <td>PN <td>TA <td>VM <td>60</td> </td></td></td></td></td></td></td>	TL <td>SL <td>PG <td>ED <td>PN <td>TA <td>VM <td>60</td> </td></td></td></td></td></td>	SL <td>PG <td>ED <td>PN <td>TA <td>VM <td>60</td> </td></td></td></td></td>	PG <td>ED <td>PN <td>TA <td>VM <td>60</td> </td></td></td></td>	ED <td>PN <td>TA <td>VM <td>60</td> </td></td></td>	PN <td>TA <td>VM <td>60</td> </td></td>	TA <td>VM <td>60</td> </td>	VM <td>60</td>	60		
QY	61	V	L	R	K	P	A	G	S	H	P	S	R	M	A	G	M	R	L	L	R	S	V	O	L	D
Db	1	MAV <td>GAL <td>TA <td>ALL <td>AA <td>LP <td>AG <td>TA <td>LP <td>RR <td>CP <td>AG <td>SV <td>AG <td>VL <td>TL <td>SL <td>PG <td>ED <td>PN <td>TA <td>VM <td>60</td> </td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td>	GAL <td>TA <td>ALL <td>AA <td>LP <td>AG <td>TA <td>LP <td>RR <td>CP <td>AG <td>SV <td>AG <td>VL <td>TL <td>SL <td>PG <td>ED <td>PN <td>TA <td>VM <td>60</td> </td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td>	TA <td>ALL <td>AA <td>LP <td>AG <td>TA <td>LP <td>RR <td>CP <td>AG <td>SV <td>AG <td>VL <td>TL <td>SL <td>PG <td>ED <td>PN <td>TA <td>VM <td>60</td> </td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td>	ALL <td>AA <td>LP <td>AG <td>TA <td>LP <td>RR <td>CP <td>AG <td>SV <td>AG <td>VL <td>TL <td>SL <td>PG <td>ED <td>PN <td>TA <td>VM <td>60</td> </td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td>	AA <td>LP <td>AG <td>TA <td>LP <td>RR <td>CP <td>AG <td>SV <td>AG <td>VL <td>TL <td>SL <td>PG <td>ED <td>PN <td>TA <td>VM <td>60</td> </td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td>	LP <td>AG <td>TA <td>LP <td>RR <td>CP <td>AG <td>SV <td>AG <td>VL <td>TL <td>SL <td>PG <td>ED <td>PN <td>TA <td>VM <td>60</td> </td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td>	AG <td>TA <td>LP <td>RR <td>CP <td>AG <td>SV <td>AG <td>VL <td>TL <td>SL <td>PG <td>ED <td>PN <td>TA <td>VM <td>60</td> </td></td></td></td></td></td></td></td></td></td></td></td></td></td></td>	TA <td>LP <td>RR <td>CP <td>AG <td>SV <td>AG <td>VL <td>TL <td>SL <td>PG <td>ED <td>PN <td>TA <td>VM <td>60</td> </td></td></td></td></td></td></td></td></td></td></td></td></td></td>	LP <td>RR <td>CP <td>AG <td>SV <td>AG <td>VL <td>TL <td>SL <td>PG <td>ED <td>PN <td>TA <td>VM <td>60</td> </td></td></td></td></td></td></td></td></td></td></td></td></td>	RR <td>CP <td>AG <td>SV <td>AG <td>VL <td>TL <td>SL <td>PG <td>ED <td>PN <td>TA <td>VM <td>60</td> </td></td></td></td></td></td></td></td></td></td></td></td>	CP <td>AG <td>SV <td>AG <td>VL <td>TL <td>SL <td>PG <td>ED <td>PN <td>TA <td>VM <td>60</td> </td></td></td></td></td></td></td></td></td></td></td>	AG <td>SV <td>AG <td>VL <td>TL <td>SL <td>PG <td>ED <td>PN <td>TA <td>VM <td>60</td> </td></td></td></td></td></td></td></td></td></td>	SV <td>AG <td>VL <td>TL <td>SL <td>PG <td>ED <td>PN <td>TA <td>VM <td>60</td> </td></td></td></td></td></td></td></td></td>	AG <td>VL <td>TL <td>SL <td>PG <td>ED <td>PN <td>TA <td>VM <td>60</td> </td></td></td></td></td></td></td></td>	VL <td>TL <td>SL <td>PG <td>ED <td>PN <td>TA <td>VM <td>60</td> </td></td></td></td></td></td></td>	TL <td>SL <td>PG <td>ED <td>PN <td>TA <td>VM <td>60</td> </td></td></td></td></td></td>	SL <td>PG <td>ED <td>PN <td>TA <td>VM <td>60</td> </td></td></td></td></td>	PG <td>ED <td>PN <td>TA <td>VM <td>60</td> </td></td></td></td>	ED <td>PN <td>TA <td>VM <td>60</td> </td></td></td>	PN <td>TA <td>VM <td>60</td> </td></td>	TA <td>VM <td>60</td> </td>	VM <td>60</td>	60		
QY	61	V	L	R	K	P	A	G	S	H	P	S	R	M	A	G	M	R	L	L	R	S	V	O	L	
Db	61	V	L	R	K	P	A	G	S	H	P	S	R	M	A	G	M	R	L	L	R	S	V	O	L	
QY	121	C	P	K	S	L	S	N	V	C	M	E	G	R	S	T	P	S	L	T	T	K	V	L	V	
Db	121	C	P	K	S	L	S	N	V	C	M	E	G	R	S	T	P	S	L	T	T	K	V	L	V	

Db 121 CFRKSPLSNVCEWBGPRSTPLTTKAVLLVRKFQNSPAEDFOEPCQYSGESQKFSQCLAV 180
Qy 181 PEDSSFYIVSMCVASSVSGSKFTQTFQCGGLQDPDPANITVTVAANPRMLSTWOD 240
Db 181 PEDSSFYIVSMCVASSVSGSKFTQTFQCGGLQDPDPANITVTVAANPRMLSTWOD 240
Qy 241 PHSWNSFYRLRFLRYRARSKTFTTMMVKDLQHHCVIHDAMSGLRHVQLRAQEEFQ 300
Db 241 PHSWNSFYRLRFLRYRARSKTFTTMMVKDLQHHCVIHDAMSGLRHVQLRAQEEFQ 300
Qy 301 GEWSESPKMGTPWTESRSPPAENESTPQALTTNKDDNLLFRDSANATSLPYEFMP 360
Db 301 GEWSESPKMGTPWTESRSPPAENESTPQALTTNKDDNLLFRDSANATSLPYEFMP 356
Qy 361 VPRGEDSKVAP 373
Db 357 ---QDSSVPLP 365

RESULT 4
5171840-2
; Patent No. 5171840
; APPLICANT: KISHIMOTO, TADAMITSU
; TITLE OF INVENTION: RECEPTOR PROTEIN FOR HUMAN B CELL
; STIMULATORY FACTOR-2
; NUMBER OF SEQUENCES: 11
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/298,694
; FILING DATE: 19-JAN-1989
; SEQ ID NO:2:
5171840-2
LENGTH: 468

Query Match 67.0%; Score 1918; DB 6; Length 468;
Best Local Similarity 96.5%; Pred. No. 1e-150;
Matches 360; Conservative 1; Mismatches 4; Indels 8; Gaps 1;
Qy 1 MNAVGCALLAALAAAGALAPRCPCPAQEVARGVLTSLPGDSVTLTCPGVEPBDNATVHM 60
Db 1 MNAVGCALLAALAAAGALAPRCPCPAQEVARGVLTSLPGDSVTLTCPGVEPBDNATVHM 60
Qy 61 VLKRPAGSHPSRMAGMGRLLRLRSVQLHDSGNVSCYRAGRPAQVHLVDPPEEPQLS 120
Db 61 VLKRPAGSHPSRMAGMGRLLRLRSVQLHDSGNVSCYRAGRPAQVHLVDPPEEPQLS 120
Qy 121 CFRKSPLSNVCEWBGPRSTPLTTKAVLLVRKFQNSPAEDFOEPCQYSGESQKFSQCLAV 180
Db 121 CFRKSPLSNVCEWBGPRSTPLTTKAVLLVRKFQNSPAEDFOEPCQYSGESQKFSQCLAV 180
Qy 181 PEDSSFYIVSMCVASSVSGSKFTQTFQCGGLQDPDPANITVTVAANPRMLSTWOD 240
Db 181 PEDSSFYIVSMCVASSVSGSKFTQTFQCGGLQDPDPANITVTVAANPRMLSTWOD 240
Qy 241 PHSWNSFYRLRFLRYRARSKTFTTMMVKDLQHHCVIHDAMSGLRHVQLRAQEEFQ 300
Db 241 PHSWNSFYRLRFLRYRARSKTFTTMMVKDLQHHCVIHDAMSGLRHVQLRAQEEFQ 300
Qy 301 GEWSESPKMGTPWTESRSPPAENESTPQALTTNKDDNLLFRDSANATSLPYEFMP 360
Db 301 GEWSESPKMGTPWTESRSPPAENESTPQALTTNKDDNLLFRDSANATSLPYEFMP 356
Qy 361 VPRGEDSKVAP 373
Db 357 ---QDSSVPLP 365

RESULT 5
5480796-2
; Patent No. 5480796
; APPLICANT: KISHIMOTO, TADAMITSU
; TITLE OF INVENTION: ANTIBODIES AGAINST THE RECEPTOR PROTEIN
; FOR HUMAN B CELL STIMULATORY FACTOR-2
; NUMBER OF SEQUENCES: 8

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/907,650
; FILING DATE: 02-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 298,694
; FILING DATE: 19-JAN-1989
; SEQ ID NO:2:
5480796-2
LENGTH: 468

Query Match 67.0%; Score 1918; DB 6; Length 468;
Best Local Similarity 96.5%; Pred. No. 1e-150;
Matches 360; Conservative 1; Mismatches 4; Indels 8; Gaps 1;
Qy 1 MNAVGCALLAALAAAGALAPRCPCPAQEVARGVLTSLPGDSVTLTCPGVEPBDNATVHM 60
Db 1 MNAVGCALLAALAAAGALAPRCPCPAQEVARGVLTSLPGDSVTLTCPGVEPBDNATVHM 60
Qy 61 VLKRPAGSHPSRMAGMGRLLRLRSVQLHDSGNVSCYRAGRPAQVHLVDPPEEPQLS 120
Db 61 VLKRPAGSHPSRMAGMGRLLRLRSVQLHDSGNVSCYRAGRPAQVHLVDPPEEPQLS 120
Qy 121 CFRKSPLSNVCEWBGPRSTPLTTKAVLLVRKFQNSPAEDFOEPCQYSGESQKFSQCLAV 180
Db 121 CFRKSPLSNVCEWBGPRSTPLTTKAVLLVRKFQNSPAEDFOEPCQYSGESQKFSQCLAV 180
Qy 181 PEDSSFYIVSMCVASSVSGSKFTQTFQCGGLQDPDPANITVTVAANPRMLSTWOD 240
Db 181 PEDSSFYIVSMCVASSVSGSKFTQTFQCGGLQDPDPANITVTVAANPRMLSTWOD 240
Qy 241 PHSWNSFYRLRFLRYRARSKTFTTMMVKDLQHHCVIHDAMSGLRHVQLRAQEEFQ 300
Db 241 PHSWNSFYRLRFLRYRARSKTFTTMMVKDLQHHCVIHDAMSGLRHVQLRAQEEFQ 300
Qy 301 GEWSESPKMGTPWTESRSPPAENESTPQALTTNKDDNLLFRDSANATSLPYEFMP 360
Db 301 GEWSESPKMGTPWTESRSPPAENESTPQALTTNKDDNLLFRDSANATSLPYEFMP 356
Qy 361 VPRGEDSKVAP 373
Db 357 ---QDSSVPLP 365

RESULT 6
US-09-313-942-15
; Sequence 15, Application US/09313942
; Patent No. 6472179
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: AND USING
; FILE REFERENCE: REG 203-A
; CURRENT APPLICATION NUMBER: US/09/313,942
; CURRENT FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-313-942-15

Query Match 66.8%; Score 1910; DB 4; Length 360;
Best Local Similarity 99.4%; Pred. No. 3.1e-150;
Matches 355; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MNAVGCALLAALAAAGALAPRCPCPAQEVARGVLTSLPGDSVTLTCPGVEPBDNATVHM 60
Db 1 MNAVGCALLAALAAAGALAPRCPCPAQEVARGVLTSLPGDSVTLTCPGVEPBDNATVHM 60

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QY 61 VLKPPAAGSHPSRWAGMRLLRSVOLHDSGNVSCYRAGRPACTVHLVDPPEEPOLS 120
DB 61 VLKPPAAGSHPSRWAGMRLLRSVOLHDSGNVSCYRAGRPACTVHLVDPPEEPOLS 120
QY 121 CFRKSPLSNVVCEWGPSTPSLTITKAVLLVRKFONSPAEDEFOEPCQYSEOSQKFSQCLAV 180
DB 121 CFRKSPLSNVVCEWGPSTPSLTITKAVLLVRKFONSPAEDEFOEPCQYSEOSQKFSQCLAV 180
QY 181 PEGDSSFYIVSMCVASSVSGSKFTQTFQCGIILQPPDPANITVTAARNPRLSVTWOD 240
DB 181 PEGDSSFYIVSMCVASSVSGSKFTQTFQCGIILQPPDPANITVTAARNPRLSVTWOD 240
QY 241 PHSNNSFFYRLRPELRYRARSKTFTTWVVKDLOHHCVIDHMSGIRHVOLRAOEFEQ 300
DB 241 PHSNNSFFYRLRPELRYRARSKTFTTWVVKDLOHHCVIDHMSGIRHVOLRAOEFEQ 300
QY 301 GEMSEMSPEAMGTPWTESRSPPAENEVSTPMQALTTNKDDNILLFRDSANATSLPVQ 357
DB 301 GEMSEMSPEAMGTPWTESRSPPAENEVSTPMQALTTNKDDNILLFRDSANATSLPVQ 357

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RESULT 7
5171840-7
; Patent No. 5171840
; APPLICANT: KISHIMOTO, TADAMITSU
; TITLE OF INVENTION: RECEPTOR PROTEIN FOR HUMAN B CELL
; STIMULATORY FACTOR-2
; NUMBER OF SEQUENCES: 11
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/298,694
; FILING DATE: 19-JAN-1989
; SEQ ID NO: 7:
; LENGTH: 344
5171840-7

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Query Match 64.7%; Score 1852; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 1.9e-145;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLAVGALLAALLAALPAGALAPRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60
DB 1 MLAVGALLAALLAALPAGALAPRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60
QY 61 VLKPPAAGSHPSRWAGMRLLRSVOLHDSGNVSCYRAGRPACTVHLVDPPEEPOLS 120
DB 61 VLKPPAAGSHPSRWAGMRLLRSVOLHDSGNVSCYRAGRPACTVHLVDPPEEPOLS 120
QY 121 CFRKSPLSNVVCEWGPSTPSLTITKAVLLVRKFONSPAEDEFOEPCQYSEOSQKFSQCLAV 180
DB 121 CFRKSPLSNVVCEWGPSTPSLTITKAVLLVRKFONSPAEDEFOEPCQYSEOSQKFSQCLAV 180
QY 181 PEGDSSFYIVSMCVASSVSGSKFTQTFQCGIILQPPDPANITVTAARNPRLSVTWOD 240
DB 181 PEGDSSFYIVSMCVASSVSGSKFTQTFQCGIILQPPDPANITVTAARNPRLSVTWOD 240
QY 241 PHSNNSFFYRLRPELRYRARSKTFTTWVVKDLOHHCVIDHMSGIRHVOLRAOEFEQ 300
DB 241 PHSNNSFFYRLRPELRYRARSKTFTTWVVKDLOHHCVIDHMSGIRHVOLRAOEFEQ 300
QY 301 GEMSEMSPEAMGTPWTESRSPPAENEVSTPMQALTTNKDDNILLFRDSANATSLPVQ 344
DB 301 GEMSEMSPEAMGTPWTESRSPPAENEVSTPMQALTTNKDDNILLFRDSANATSLPVQ 344

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RESULT 8
5480796-7
; Patent No. 5480796
; APPLICANT: KISHIMOTO, TADAMITSU
; TITLE OF INVENTION: ANTIBODIES AGAINST THE RECEPTOR PROTEIN
; FOR HUMAN B CELL STIMULATORY FACTOR-2
; NUMBER OF SEQUENCES: 8
; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/07/907,650
; FILING DATE: 02-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 298,694
; FILING DATE: 19-JAN-1989
; SEQ ID NO: 7:
; LENGTH: 344
5480796-7

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Query Match 64.7%; Score 1852; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 1.9e-145;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLAVGALLAALLAALPAGALAPRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60
DB 1 MLAVGALLAALLAALPAGALAPRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60
QY 61 VLKPPAAGSHPSRWAGMRLLRSVOLHDSGNVSCYRAGRPACTVHLVDPPEEPOLS 120
DB 61 VLKPPAAGSHPSRWAGMRLLRSVOLHDSGNVSCYRAGRPACTVHLVDPPEEPOLS 120
QY 121 CFRKSPLSNVVCEWGPSTPSLTITKAVLLVRKFONSPAEDEFOEPCQYSEOSQKFSQCLAV 180
DB 121 CFRKSPLSNVVCEWGPSTPSLTITKAVLLVRKFONSPAEDEFOEPCQYSEOSQKFSQCLAV 180
QY 181 PEGDSSFYIVSMCVASSVSGSKFTQTFQCGIILQPPDPANITVTAARNPRLSVTWOD 240
DB 181 PEGDSSFYIVSMCVASSVSGSKFTQTFQCGIILQPPDPANITVTAARNPRLSVTWOD 240
QY 241 PHSNNSFFYRLRPELRYRARSKTFTTWVVKDLOHHCVIDHMSGIRHVOLRAOEFEQ 300
DB 241 PHSNNSFFYRLRPELRYRARSKTFTTWVVKDLOHHCVIDHMSGIRHVOLRAOEFEQ 300
QY 301 GEMSEMSPEAMGTPWTESRSPPAENEVSTPMQALTTNKDDNILLFRDSANATSLPVQ 344
DB 301 GEMSEMSPEAMGTPWTESRSPPAENEVSTPMQALTTNKDDNILLFRDSANATSLPVQ 344

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RESULT 9
US-09-313-942-26
; Sequence 26, Application US/09313942
; Patent No. 6472179
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-A
; CURRENT APPLICATION NUMBER: US/09/313,942
; CURRENT FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 1158
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-313-942-26

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Query Match 62.5%; Score 1788; DB 4; Length 1158;
Best Local Similarity 99.1%; Pred. No. 2.4e-139;
Matches 331; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLAVGALLAALLAALPAGALAPRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60
DB 1 MLAVGALLAALLAALPAGALAPRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60
QY 61 VLKPPAAGSHPSRWAGMRLLRSVOLHDSGNVSCYRAGRPACTVHLVDPPEEPOLS 120
DB 61 VLKPPAAGSHPSRWAGMRLLRSVOLHDSGNVSCYRAGRPACTVHLVDPPEEPOLS 120

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QY 121 CFFKSPLSNVVCEWGRSTPSLTITKAVLVKRFQNSPAEDFOBPQCOYSQSFSCQLAV 180
 DB 121 CFFKSPLSNVVCEWGRSTPSLTITKAVLVKRFQNSPAEDFOBPQCOYSQSFSCQLAV 180
 QY 181 PEGDSSFYIVSMCVASVSGSKFSKTQTFQCGGILQDPDPANITVTAVANPRLSVTWOD 240
 DB 181 PEGDSSFYIVSMCVASVSGSKFSKTQTFQCGGILQDPDPANITVTAVANPRLSVTWOD 240
 QY 241 PHSWNSFYRLRFLRYRAERSKTFTTMMVKDLOHHCVIDAMSGLRHVVLRAOEFGQ 300
 DB 241 PHSWNSFYRLRFLRYRAERSKTFTTMMVKDLOHHCVIDAMSGLRHVVLRAOEFGQ 300
 QY 301 GEWSEWSPAMGTPWTESRSPPAENEVSITPM 334
 DB 301 GEWSEWSPAMGTPWTESRSPPAENEVSITPM 334

RESULT 10

US-09-313-942-24
 ; Sequence 24, Application US/09313942
 ; Patent No. 6472179
 ; GENERAL INFORMATION:
 ; APPLICANT: REGENERON PHARMACEUTICALS, INC.
 ; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
 ; TITLE OF INVENTION: AND USING
 ; FILE REFERENCE: REG 203-A
 ; CURRENT APPLICATION NUMBER: US/09/313,942
 ; CURRENT FILING DATE: 1999-05-19
 ; PRIOR APPLICATION NUMBER: 09/313,942
 ; PRIOR FILING DATE: 1999-05-19
 ; PRIOR APPLICATION NUMBER: 60/101,858
 ; PRIOR FILING DATE: 1998-09-25
 ; NUMBER OF SEQ ID NOS: 32
 ; SOFTWARE: FASTSEQ for Windows Version 3.0
 ; SEQ ID NO 24
 ; LENGTH: 1168
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-313-942-24

Query Match 62.3%; Score 1783; DB 4; Length 1168;
 Best Local Similarity 99.7%; Pred. No. 6.2e-139;
 Matches 330; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAAVGCALLAALLAAGALAPRCPCAOEVARGVLTSLPDSVTTLTCPGVEPDNATVHW 60
 DB 1 MAAVGCALLAALLAAGALAPRCPCAOEVARGVLTSLPDSVTTLTCPGVEPDNATVHW 60
 QY 61 VLKRPAGSHPSRMAGMGRRLILRSVQLHDSGNYSCYRAGRPAQTVHLLVDVPEEPQLS 120
 DB 61 VLKRPAGSHPSRMAGMGRRLILRSVQLHDSGNYSCYRAGRPAQTVHLLVDVPEEPQLS 120
 QY 121 CFFKSPLSNVVCEWGRSTPSLTITKAVLVKRFQNSPAEDFOBPQCOYSQSFSCQLAV 180
 DB 121 CFFKSPLSNVVCEWGRSTPSLTITKAVLVKRFQNSPAEDFOBPQCOYSQSFSCQLAV 180
 QY 181 PEGDSSFYIVSMCVASVSGSKFSKTQTFQCGGILQDPDPANITVTAVANPRLSVTWOD 240
 DB 181 PEGDSSFYIVSMCVASVSGSKFSKTQTFQCGGILQDPDPANITVTAVANPRLSVTWOD 240
 QY 241 PHSWNSFYRLRFLRYRAERSKTFTTMMVKDLOHHCVIDAMSGLRHVVLRAOEFGQ 300
 DB 241 PHSWNSFYRLRFLRYRAERSKTFTTMMVKDLOHHCVIDAMSGLRHVVLRAOEFGQ 300
 QY 301 GEWSEWSPAMGTPWTESRSPPAENEVSITPM 331
 DB 301 GEWSEWSPAMGTPWTESRSPPAENEVSITPM 331

RESULT 11
 5171840-6
 ; Patent No. 5171840
 ; APPLICANT: KISHIMOTO, TADAMITSU

; TITLE OF INVENTION: RECEPTOR PROTEIN FOR HUMAN B CELL
 ; STIMULATORY FACTOR-2
 ; NUMBER OF SEQUENCES: 11
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/298,694
 ; FILING DATE: 19-JAN-1989
 ; SEQ ID NO: 6
 ; LENGTH: 323
 5171840-6

Query Match 60.9%; Score 1741; DB 6; Length 323;
 Best Local Similarity 100.0%; Pred. No. 2.8e-136;
 Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAVGCALLAALLAAGALAPRCPCAOEVARGVLTSLPDSVTTLTCPGVEPDNATVHW 60
 DB 1 MAAVGCALLAALLAAGALAPRCPCAOEVARGVLTSLPDSVTTLTCPGVEPDNATVHW 60
 QY 61 VLKRPAGSHPSRMAGMGRRLILRSVQLHDSGNYSCYRAGRPAQTVHLLVDVPEEPQLS 120
 DB 61 VLKRPAGSHPSRMAGMGRRLILRSVQLHDSGNYSCYRAGRPAQTVHLLVDVPEEPQLS 120
 QY 121 CFFKSPLSNVVCEWGRSTPSLTITKAVLVKRFQNSPAEDFOBPQCOYSQSFSCQLAV 180
 DB 121 CFFKSPLSNVVCEWGRSTPSLTITKAVLVKRFQNSPAEDFOBPQCOYSQSFSCQLAV 180
 QY 181 PEGDSSFYIVSMCVASVSGSKFSKTQTFQCGGILQDPDPANITVTAVANPRLSVTWOD 240
 DB 181 PEGDSSFYIVSMCVASVSGSKFSKTQTFQCGGILQDPDPANITVTAVANPRLSVTWOD 240
 QY 241 PHSWNSFYRLRFLRYRAERSKTFTTMMVKDLOHHCVIDAMSGLRHVVLRAOEFGQ 300
 DB 241 PHSWNSFYRLRFLRYRAERSKTFTTMMVKDLOHHCVIDAMSGLRHVVLRAOEFGQ 300
 QY 301 GEWSEWSPAMGTPWTESRSP 322
 DB 301 GEWSEWSPAMGTPWTESRSP 322

RESULT 12
 5480796-6
 ; Patent No. 5480796
 ; APPLICANT: KISHIMOTO, TADAMITSU
 ; TITLE OF INVENTION: ANTIBODIES AGAINST THE RECEPTOR PROTEIN
 ; FOR HUMAN B CELL STIMULATORY FACTOR-2
 ; NUMBER OF SEQUENCES: 8
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/907,650
 ; FILING DATE: 02-JUL-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 298,694
 ; FILING DATE: 19-JAN-1989
 ; SEQ ID NO: 6
 ; LENGTH: 323
 5480796-6

Query Match 60.9%; Score 1741; DB 6; Length 323;
 Best Local Similarity 100.0%; Pred. No. 2.8e-136;
 Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAVGCALLAALLAAGALAPRCPCAOEVARGVLTSLPDSVTTLTCPGVEPDNATVHW 60
 DB 1 MAAVGCALLAALLAAGALAPRCPCAOEVARGVLTSLPDSVTTLTCPGVEPDNATVHW 60
 QY 61 VLKRPAGSHPSRMAGMGRRLILRSVQLHDSGNYSCYRAGRPAQTVHLLVDVPEEPQLS 120
 DB 61 VLKRPAGSHPSRMAGMGRRLILRSVQLHDSGNYSCYRAGRPAQTVHLLVDVPEEPQLS 120
 QY 121 CFFKSPLSNVVCEWGRSTPSLTITKAVLVKRFQNSPAEDFOBPQCOYSQSFSCQLAV 180
 DB 121 CFFKSPLSNVVCEWGRSTPSLTITKAVLVKRFQNSPAEDFOBPQCOYSQSFSCQLAV 180
 QY 181 PEGDSSFYIVSMCVASVSGSKFSKTQTFQCGGILQDPDPANITVTAVANPRLSVTWOD 240
 DB 181 PEGDSSFYIVSMCVASVSGSKFSKTQTFQCGGILQDPDPANITVTAVANPRLSVTWOD 240

```

Db      181 PEGDSSFYIVSMCVASSVSGSKSTQTFQCGGILPDPPANITVTAVARNPRLSVTMQD 240
QY      241 PHSNNSFYRLRFEFLRYARERKSTTTMMVVDLQHCVTHDAMSGLRHVYQLRAOEFGQ 300
Db      241 PHSNNSFYRLRFEFLRYARERKSTTTMMVVDLQHCVTHDAMSGLRHVYQLRAOEFGQ 300
QY      301 GEWSEMSPEAMGTPTWESRSP 322
Db      301 GEWSEMSPEAMGTPTWESRSP 322

```

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RESULT 13
US-09-313-942-16
; Sequence 16, Application US/09313942
; Patent No. 6472179
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-A
; CURRENT APPLICATION NUMBER: US/09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 315
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-313-942-16

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Query Match      58.8%; Score 1683; DB 4; Length 315;
Best Local Similarity 99.7%; Pred. No. 1.8e-131;
Matches 312; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY      1  MLAVGALLAALAAPGAAALAPRRCPAEOVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60
Db      1  MVAAGCALLAALAAPGAAALAPRRCPAEOVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60
QY      61 VLKPAAGSHPSRWAGMGRLLRSVQLHDSGNVSCYRAGRPAQTVHLVDVPEEPQLS 120
Db      61 VLKPAAGSHPSRWAGMGRLLRSVQLHDSGNVSCYRAGRPAQTVHLVDVPEEPQLS 120
QY      121 CFRKSPLSNVVCEWGPSTSLTTKAVLVKRFQNSPAEDFOEPQOYSQESQKFSQCLAV 180
Db      121 CFRKSPLSNVVCEWGPSTSLTTKAVLVKRFQNSPAEDFOEPQOYSQESQKFSQCLAV 180
QY      181 PEGDSSFYIVSMCVASSVSGSKSTQTFQCGGILPDPPANITVTAVARNPRLSVTMQD 240
Db      181 PEGDSSFYIVSMCVASSVSGSKSTQTFQCGGILPDPPANITVTAVARNPRLSVTMQD 240
QY      241 PHSNNSFYRLRFEFLRYARERKSTTTMMVVDLQHCVTHDAMSGLRHVYQLRAOEFGQ 300
Db      241 PHSNNSFYRLRFEFLRYARERKSTTTMMVVDLQHCVTHDAMSGLRHVYQLRAOEFGQ 300
QY      301 GEWSEMSPEAMGT 313
Db      301 GEWSEMSPEAMGT 313

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RESULT 14
5171840-5
; Patent No. 5171840
; APPLICANT: KISHIMOTO, TADAMITSU
; TITLE OF INVENTION: RECEPTOR PROTEIN FOR HUMAN B CELL
; STIMULATORY FACTOR-2
; NUMBER OF SEQUENCES: 11
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/298,694

```

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; FILING DATE: 19-JAN-1989
; SEQ ID NO: 5
; LENGTH: 386
5171840-5

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Query Match      48.5%; Score 1389; DB 6; Length 386;
Best Local Similarity 73.6%; Pred. No. 5.9e-107;
Matches 276; Conservative 1; Mismatches 4; Indels 94; Gaps 4;

```

```

QY      1  MLAVGALLAALAAPGAAALAPRRCPAEOVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60
Db      1  MLAVGALLAALAAPGAAALAPRRCPA-----
QY      61 VLKPAAGSHPSRWAGMGRLLRSVQLHDSGNVSCYRAGRPAQTVHLVDVPEEPQLS 120
Db      61 VLKPAAGSHPSRWAGMGRLLRSVQLHDSGNVSCYRAGRPAQTVHLVDVPEEPQLS 120
QY      121 CFRKSPLSNVVCEWGPSTSLTTKAVLVKRFQNSPAEDFOEPQOYSQESQKFSQCL 178
Db      121 CFRKSPLSNVVCEWGPSTSLTTKAVLVKRFQNSPAEDFOEPQOYSQESQKFSQCL 178
QY      179 AVEGDSSFYIVSMCVASSVSGSKSTQTFQCGGILPDPPANITVTAVARNPRLSVTM 238
Db      179 AVEGDSSFYIVSMCVASSVSGSKSTQTFQCGGILPDPPANITVTAVARNPRLSVTM 238
QY      239 ODRHSNNSFYRLRFEFLRYARERKSTTTMMVVDLQHCVTHDAMSGLRHVYQLRAOEFP 298
Db      239 ODRHSNNSFYRLRFEFLRYARERKSTTTMMVVDLQHCVTHDAMSGLRHVYQLRAOEFP 298
QY      299 GQGEWSEMSPEAMGTPTWESRSPPAENEYSTPMQALTNKDDNITLFRDSANATSLPVEF 358
Db      299 GQGEWSEMSPEAMGTPTWESRSPPAENEYSTPMQALTNKDDNITLFRDSANATSLPVEF 358
QY      359 MEVPEGEDEKDYAAP 373
Db      359 MEVPEGEDEKDYAAP 373
QY      275 -----QDSSSVPLP 283
Db      275 -----QDSSSVPLP 283

```

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RESULT 15
5480796-5
; Patent No. 5480796
; APPLICANT: KISHIMOTO, TADAMITSU
; TITLE OF INVENTION: ANTIBODIES AGAINST THE RECEPTOR PROTEIN
; FOR HUMAN B CELL STIMULATORY FACTOR-2
; NUMBER OF SEQUENCES: 8
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/907,650
; FILING DATE: 02-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 298,694
; FILING DATE: 19-JAN-1989
; SEQ ID NO: 5
; LENGTH: 386
5480796-5

```

```

Query Match      48.5%; Score 1389; DB 6; Length 386;
Best Local Similarity 73.6%; Pred. No. 5.9e-107;
Matches 276; Conservative 1; Mismatches 4; Indels 94; Gaps 4;

```

```

QY      1  MLAVGALLAALAAPGAAALAPRRCPAEOVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60
Db      1  MLAVGALLAALAAPGAAALAPRRCPA-----
QY      61 VLKPAAGSHPSRWAGMGRLLRSVQLHDSGNVSCYRAGRPAQTVHLVDVPEEPQLS 120
Db      61 VLKPAAGSHPSRWAGMGRLLRSVQLHDSGNVSCYRAGRPAQTVHLVDVPEEPQLS 120
QY      121 CFRKSPLSNVVCEWGPSTSLTTKAVLVKRFQNSPAEDFOEPQOYSQESQKFSQCL 178
Db      121 CFRKSPLSNVVCEWGPSTSLTTKAVLVKRFQNSPAEDFOEPQOYSQESQKFSQCL 178
QY      179 AVEGDSSFYIVSMCVASSVSGSKSTQTFQCGGILPDPPANITVTAVARNPRLSVTM 238
Db      179 AVEGDSSFYIVSMCVASSVSGSKSTQTFQCGGILPDPPANITVTAVARNPRLSVTM 238

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DB 97 AVEGDSSFYIVSMCVASSVSGSKFKSTQTFQGGCIIQDPDPANITVTAVARNRMLSVTM 156
QY 239 QDPHSNNSFYRLRFELRYAERSKTFTTMVMDLQHCYIHAWGSLRHVVQLRAOEER 298
DB 157 QDPHSNNSFYRLRFELRYAERSKTFTTMVMDLQHCYIHAWGSLRHVVQLRAOEER 216
QY 299 GQGEWSEWSPAMGTPTWESRSPAPENEVSTPMQALTNNKDDNILEFRSANATSLPVER 358
DB 217 GQGEWSEWSPAMGTPTWESRSPAPENEVSTPMQALTNNKDDNILEFRSANATSLPVER 274
QY 359 MPVPEGDSKDYAAP 373
DB 275 -----QDSSSVLP 283

RESULT 16
US-09-043-785-1
; Sequence 1, Application US/09043785
; Patent No. 6172042
; GENERAL INFORMATION:
; APPLICANT: CHEBATH, Judith
; APPLICANT: HALIMI, Hubert
; APPLICANT: REVEL, Michel
; TITLE OF INVENTION: SYNTHETIC PEPTIDES THAT INHIBIT IL-6 ACTIVITY
; FILE REFERENCE: Chebath-1
; CURRENT APPLICATION NUMBER: US/09/043, 785
; EARLIER FILING DATE: 1998-09-02
; EARLIER APPLICATION NUMBER: PCT/1196/00119
; EARLIER FILING DATE: 1996-09-26
; EARLIER APPLICATION NUMBER: 115,453
; EARLIER FILING DATE: 1995-09-26
; EARLIER APPLICATION NUMBER: 118,097
; EARLIER FILING DATE: 1996-05-01
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Human
US-09-043-785-1

Query Match 40.3%; Score 1153; DB 3; Length 210;
Best Local Similarity 100.0%; Pred. No. 9, 2e-88;
Matches 210; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 113 PPEEPOLSCFRKSPISNVCEWGPSTPSLTITKAVILVRKFNQSPADPQEPQYQESQ 172
DB 1 PPEEPOLSCFRKSPISNVCEWGPSTPSLTITKAVILVRKFNQSPADPQEPQYQESQ 60
QY 173 KSCCOLAVEGDSSEFYIVSMCVASSVSGSKFKSTQTFQGGCIIQDPDPANITVTAVARNR 232
DB 61 KSCCOLAVEGDSSEFYIVSMCVASSVSGSKFKSTQTFQGGCIIQDPDPANITVTAVARNR 120
QY 233 WLSVTWQDPHSNNSFYRLRFELRYAERSKTFTTMVMDLQHCYIHAWGSLRHVVQL 292
DB 121 WLSVTWQDPHSNNSFYRLRFELRYAERSKTFTTMVMDLQHCYIHAWGSLRHVVQL 180
QY 293 RAQEEFGQGEWSEWSPAMGTPTWESRSP 322
DB 181 RAQEEFGQGEWSEWSPAMGTPTWESRSP 210

RESULT 17
5171840-11
; Patent No. 5171840
; APPLICANT: KISHIMOTO, TADAMITSU
; TITLE OF INVENTION: RECEPTOR PROTEIN FOR HUMAN B CELL
; STIMULATORY FACTOR-2
; NUMBER OF SEQUENCES: 11
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/298, 694
; FILING DATE: 19-JAN-1989
; SEQ ID NO:11;

LENGTH: 201
5171840-11
Query Match 33.2%; Score 950; DB 6; Length 201;
Best Local Similarity 89.1%; Pred. No. 6e-71;
Matches 179; Conservative 1; Mismatches 21; Indels 0; Gaps 0;
QY 123 RKSPLSNVCEWGPSTPSLTITKAVILVRKFNQSPADPQEPQYQESQKFSQCOLAVE 182
DB 1 RKSPLSNVCEWGPSTPSLTITKAVILVRKFNQSPADPQEPQYQESQKFSQCOLAVE 60
QY 183 GDSSEFYIVSMCVASSVSGSKFKSTQTFQGGCIIQDPDPANITVTAVARNRMLSVTMQDPH 242
DB 61 GDSSEFYIVSMCVASSVSGSKFKSTQTFQGGCIIQDPDPANITVTAVARNRMLSVTMQDPH 120
QY 243 SNNSFYRLRFELRYAERSKTFTTMVMDLQHCYIHAWGSLRHVVQLRAOEFGQGE 302
DB 121 SNNSFYRLRFELRYAERSKTFTTMVMDLQHCYIHAWGSLRHVVQLRAOEFGQGE 180
QY 303 WSEWSPAMGTPTWESRSPPA 323
DB 181 WSEWSPAMGTPTWESRSPPA 201

RESULT 18
US-08-716-317-7
; Sequence 7, Application US/08716317
; Patent No. 5919654
; GENERAL INFORMATION:
; APPLICANT: HAMA, YUKO
; APPLICANT: TOHDA, HIDEKI
; APPLICANT: TSUKAMOTO, HIROKO
; APPLICANT: NIKAIKO, KIYOKAZU
; APPLICANT: KIMAGAI, HIROMICHI
; TITLE OF INVENTION: SECRETION SIGNAL GENE AND EXPRESSION
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER & NEUSTADT,
; ADDRESS: P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/716,317
; FILING DATE: 02-OCT-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP96/00198
; FILING DATE: 01-FEB-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 17167/1995
; FILING DATE: 03-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 59-924-0 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 185 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

MOLECULE TYPE: peptide
US-08-716-317-7

Query Match 32.8%; Score 939; DB 2; Length 185;
Best Local Similarity 100.0%; Pred. No. 4,4e-70;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 359 MPVPPGSDSKDVAAPHROPLTSSERIDKQIRYIIDGISALRKETCNKSNMCESSKEALAE 418
DB 1 MPVPPGSDSKDVAAPHROPLTSSERIDKQIRYIIDGISALRKETCNKSNMCESSKEALAE 60

QY 419 NNINLPMAEKDGCFOGPFNEETCLVKIITGLLEFVYLYLQNRFFSSSEQARAQVOMST 478
DB 61 NNINLPMAEKDGCFOGPFNEETCLVKIITGLLEFVYLYLQNRFFSSSEQARAQVOMST 120

QY 479 KVLIOPLQKAKNLDATITPDPTTNASLITKLOQONQWLODMTHLILRSFKERLOSSLR 538
DB 121 KVLIOPLQKAKNLDATITPDPTTNASLITKLOQONQWLODMTHLILRSFKERLOSSLR 180

QY 539 ALRQM 543
DB 181 ALRQM 185

RESULT 19
US-08-792-019B-9
Sequence 9, Application US/08792019B
Patent No. 5741772

GENERAL INFORMATION:
APPLICANT: CHANG, MING-SHI
TITLE OF INVENTION: THE NEUTROTROPIC FACTOR NNT-1
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMGEN INC.
STREET: 1840 DEHAVILLAND DRIVE
CITY: THOUSAND OAKS
STATE: CA
COUNTRY: USA
ZIP: 91320

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/792.019B
FILING DATE: 03-FEB-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: COOK, ROBERT R.
REGISTRATION NUMBER: 31,602
REFERENCE/DOCKET NUMBER: A-442
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..182
NAME/KEY: Region
LOCATION: -30..0
US-08-792-019B-9

Query Match 32.8%; Score 938.5; DB 1; Length 212;
Best Local Similarity 97.9%; Pred. No. 5.9e-70;
Matches 187; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 354 LPVEF-MPVPPGSDSKDVAAPHROPLTSSERIDKQIRYIIDGISALRKETCNKSNMCESS 412
DB 1 LPVEF-MPVPPGSDSKDVAAPHROPLTSSERIDKQIRYIIDGISALRKETCNKSNMCESS 412

DB 22 LPAPFAPVPPGSDSKDVAAPHROPLTSSERIDKQIRYIIDGISALRKETCNKSNMCESS 81
QY 413 KEALAEENNINLPMAEKDGCFOGPFNEETCLVKIITGLLEFVYLYLQNRFFSSSEQAR 472
DB 82 KEALAEENNINLPMAEKDGCFOGPFNEETCLVKIITGLLEFVYLYLQNRFFSSSEQAR 141

QY 473 AVQMSKTVLIQFLOKAKNLDATITPDPTTNASLITKLOQONQWLODMTHLILRSFKER 532
DB 142 AVQMSKTVLIQFLOKAKNLDATITPDPTTNASLITKLOQONQWLODMTHLILRSFKER 201

QY 533 LOSSLRALRQM 543
DB 202 LOSSLRALRQM 212

RESULT 20
US-08-988-819-9
Sequence 9, Application US/08988819
Patent No. 6054294

GENERAL INFORMATION:
APPLICANT: CHANG, MING-SHI
TITLE OF INVENTION: NEUTROTROPIC FACTOR NNT-1
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMGEN INC.
STREET: ONE AMGEN CENTER DRIVE
CITY: THOUSAND OAKS
STATE: CA
COUNTRY: USA
ZIP: 91320

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/988.819
FILING DATE: 12-DEC-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/792.019
FILING DATE: 03-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: COOK, ROBERT R.
REGISTRATION NUMBER: 31,602
REFERENCE/DOCKET NUMBER: A-442A
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..182
NAME/KEY: Region
LOCATION: -30..0
US-08-988-819-9

Query Match 32.8%; Score 938.5; DB 3; Length 212;
Best Local Similarity 97.9%; Pred. No. 5.9e-70;
Matches 187; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 354 LPVEF-MPVPPGSDSKDVAAPHROPLTSSERIDKQIRYIIDGISALRKETCNKSNMCESS 412
DB 22 LPAPFAPVPPGSDSKDVAAPHROPLTSSERIDKQIRYIIDGISALRKETCNKSNMCESS 81

QY 413 KEALAEENNINLPMAEKDGCFOGPFNEETCLVKIITGLLEFVYLYLQNRFFSSSEQAR 472
DB 82 KEALAEENNINLPMAEKDGCFOGPFNEETCLVKIITGLLEFVYLYLQNRFFSSSEQAR 141

Qy	473	AVOMSTRKVLQFLOKAKXULDAITTPDPPTNASLITKLOAONOMLODMTHILIRSRKEF	532
	142	AVOMSTRKVLQFLOKAKXULDAITTPDPPTNASLITKLOAONOMLODMTHILIRSRKEF	201
Db			
Qy	533	LOSSLRALROM	543
Db	202	LOSSLRALROM	212

```

RESULT 21
US-09-016-534-9
; Sequence 9, Application US/09016534
; Patent No. 6143874
; General Information:
; APPLICANT: CHANG, MING-SHI
; APPLICANT: ELIOTT, GARY S.
; APPLICANT: SARMIENTO, ULLA
; APPLICANT: SEVARDI, GIORGIO
; TITLE OF INVENTION: THE NEUROTROPHIC FACTOR NNT-
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMGEN INC.
; STREET: ONE AMGEN CENTER
; CITY: THOUSAND OAKS
; STATE: CA
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,534
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/792,019
; FILING DATE: 03-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: COOK, ROBERT R.
; REGISTRATION NUMBER: 31,602
; REFERENCE/DOCKET NUMBER: A-442B
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 212 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..182
; FEATURE:
; NAME/KEY: Region
; LOCATION: -30..0
; US-09-016-534-9

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Query Match	32.8%	Score 938.5	DB 3:	Length 212:
Best Local Similarity	97.9%	Pred. No.5.9e-70:		
Matches 187:	Conservative	0	Mismatches 3:	Indels 1: Gaps 1
QY	354	L.PVEF-MVPPGEGDSKDVAAPHROPULTSSERIDKOIRYILDGISAARKETCKSNMCESS	412	
Db	22	LPAAPFAPVPPGEGDSKDVAAPHROPULTSSERIDKOIRYILDGISAARKETCKSNMCESS	81	
QY	413	KEALAENNLLNPKAEKDCGCGFSGNEETCLVYKIIITGLIEFVYLYEYLNPPESSEBOAR	472	
Db	82	KEALAENNLLNPKAEKDCGCGFSGNEETCLVYKIIITGLIEFVYLYEYLNPPESSEBOAR	141	
QY	473	AVOMSTKYLIDFLOKKAKNLDAITPDDPTNASLLTKLOAQONQMLQDMTHHLLSPKEF	532	
Db	142	AVOMSTKYLIDFLOKKAKNLDAITPDDPTNASLLTKLOAQONQMLQDMTHHLLSPKEF	201	

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Cy      533  LOSSR1ALR0M 543
      |||||
Db      202  LOSSR1ALR0M 212

      RESULT 22
      US-08-097-869-7
      Sequence 7, Application US/08097869
      Patent No. 6204364
      GENERAL INFORMATION:
      APPLICANT: Todaro, George J.
      APPLICANT: Rose, Timothy M.
      TITLE OF INVENTION: HYBRID CYTOKINES
      NUMBER OF SEQUENCES: 8
      CORRESPONDENCE ADDRESS:
      ADDRESSEE: Morrison & Foerster
      STREET: 545 Middlefield Road, Suite 200
      CITY: Menlo Park
      STATE: California
      COUNTRY: USA
      ZIP: 94025
      COMPUTER READABLE FORM:
      MEDIUM TYPE: Floppy disk
      COMPUTER: IBM PC compatible
      OPERATING SYSTEM: PC-DOS/MS-DOS
      SOFTWARE: Patent in Release #1.0, Version #1.25
      CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US/08/097,869
      FILING DATE:
      CLASSIFICATION: 530
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US 07/753,178
      FILING DATE: 30-AUG-1991
      ATTORNEY/AGENT INFORMATION:
      NAME: Murashige, Kate H.
      REGISTRATION NUMBER: 29,959
      REFERENCE/DOCKET NUMBER: 24455-20001.00
      TELECOMMUNICATION INFORMATION:
      TELEPHONE: 415-813-5600
      TELEFAX: 415-327-2951
      TELEX: 706141
      INFORMATION FOR SEQ ID NO: 7:
      SEQUENCE CHARACTERISTICS:
      LENGTH: 212 amino acids
      TYPE: amino acid
      STRANDEDNESS: single
      TOPOLOGY: linear
      US-08-097-869-7

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Query Match	32.8%	Score 938.5	DB 3	Length 212
Best Local Similarity	97.9%	Pred. No. 5,9e-70		
Matches	187	Conservative	0	Mismatches 3
				Indels 1
				Gaps 1
QY	354	LPVEF-MPVPPEGDSKVVAAPHROPLTSSERIDKQIRIYIIIDGISALKEFTCNKSNMCESS	412	
Db	22	LPAFPAPVPBPGEBSKVVAAPHROPLTSSERIDKQIRIYIIIDGISALKEFTCNKSNMCESS	81	
QY	413	KEALAEANNLNPVKAEKDGCFQSGFNEETCLVKIITGLTFEVEVLYLQNRFSSESEQAR	472	
Db	82	KEALAEANNLNPVKAEKDGCFQSGFNEETCLVKIITGLTFEVEVLYLQNRFSSESEQAR	141	
QY	473	AVQNSTKYLIOFLQKAKNLDATITPPTTNASILITLQAOQNMQLDMTHLILRSKEF	532	
Db	142	AVQNSTKYLIOFLQKAKNLDATITPPTTNASILITLQAOQNMQLDMTHLILRSKEF	201	
QY	533	LOSSLRALRQW 543		
Db	202	LOSSLRALRQW 212		

Db 142 AVOMSTKVLIOFLQKAKNDAITTPDPTTNASLITKLOAONQWLODMTHILRSFKF 201
QY 533 LOSSLRALROM 543
Db 202 LOSSLRALROM 212

RESULT 26

US-09-439-856-6
; Sequence 6, Application US/09439856
; Patent No. 641009
; GENERAL INFORMATION:
; APPLICANT: Galun, Etchan
; APPLICANT: Nahot, Orit
; APPLICANT: Blum, Herbert E.
; TITLE OF INVENTION: A Pharmaceutical Composition for Treating
; TITLE OF INVENTION: Hepatitis B Virus (HBV) Infection
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Davidson, Davidson and Kappel, LLC
; STREET: 1140 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS-DOS EDITOR
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/439,856
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/795,473
; FILING DATE: 11-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Davidson, Clifford M.
; REGISTRATION NUMBER: 32,728
; REFERENCE/DOCKET NUMBER: 963,1007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)-997-1028
; TELEFAX: (212)-997-1037
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 212 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; US-09-439-856-6

Query Match 32.8%; Score 938.5; DB 4; Length 212;
Best Local Similarity 97.9%; Pred. No. 5.9e-70;
Matches 187; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 354 LPVEF-MPVPGSDSDVAAPHROPLTSSERIDKOIRYILDGISAIRKETCNKSNKNCSS 412
Db 22 LPAAPAPVPBGSDSDVAAPHROPLTSSERIDKOIRYILDGISAIRKETCNKSNKNCSS 81
QY 413 KEALAENNINLPRMAEKDCFGSGFNEETCLVKIITGLLEFEVYLEYLONRFSSSEQAR 472
Db 82 KEALAENNINLPRMAEKDCFGSGFNEETCLVKIITGLLEFEVYLEYLONRFSSSEQAR 141
QY 473 AVOMSTKVLIOFLQKAKNDAITTPDPTTNASLITKLOAONQWLODMTHILRSFKF 532
Db 142 AVOMSTKVLIOFLQKAKNDAITTPDPTTNASLITKLOAONQWLODMTHILRSFKF 201
QY 533 LOSSLRALROM 543
Db 202 LOSSLRALROM 212

RESULT 27

US-09-462-941-13
; Sequence 13, Application US/09462941
; Patent No. 6608183
; GENERAL INFORMATION:
; APPLICANT: Cox III, George N.
; APPLICANT: Bolder Biotechnology, Inc.
; TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
; FILE REFERENCE: 4152-1-PUS
; CURRENT APPLICATION NUMBER: US/09/462,941
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/052,516
; PRIOR FILING DATE: 1997-07-14
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 13
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-462-941-13

Query Match 32.8%; Score 938.5; DB 4; Length 212;
Best Local Similarity 97.9%; Pred. No. 5.9e-70;
Matches 187; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 354 LPVEF-MPVPGSDSDVAAPHROPLTSSERIDKOIRYILDGISAIRKETCNKSNKNCSS 412
Db 22 LPAAPAPVPBGSDSDVAAPHROPLTSSERIDKOIRYILDGISAIRKETCNKSNKNCSS 81
QY 413 KEALAENNINLPRMAEKDCFGSGFNEETCLVKIITGLLEFEVYLEYLONRFSSSEQAR 472
Db 82 KEALAENNINLPRMAEKDCFGSGFNEETCLVKIITGLLEFEVYLEYLONRFSSSEQAR 141
QY 473 AVOMSTKVLIOFLQKAKNDAITTPDPTTNASLITKLOAONQWLODMTHILRSFKF 532
Db 142 AVOMSTKVLIOFLQKAKNDAITTPDPTTNASLITKLOAONQWLODMTHILRSFKF 201
QY 533 LOSSLRALROM 543
Db 202 LOSSLRALROM 212

RESULT 28
5510472-2
; Patent No. 5510472
; APPLICANT: REVEL, MICHEL; TIOLLAIS, PIERRE
; TITLE OF INVENTION: PRODUCTION OF RECOMBINANT HUMAN
; INTERFERON-BETA2
; NUMBER OF SEQUENCES: 9
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/883,633
; FILING DATE: 15-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 208,925
; FILING DATE: 20-NOV-1980
; APPLICATION NUMBER: 449,447
; FILING DATE: 12-DEC-1989
; APPLICATION NUMBER: 860,883
; FILING DATE: 08-MAY-1986
; APPLICATION NUMBER: 208,925
; FILING DATE: 20-NOV-1980
; SEQ ID NO: 2
; LENGTH: 212
5510472-2

Query Match 32.8%; Score 938.5; DB 6; Length 212;
Best Local Similarity 97.9%; Pred. No. 5.9e-70;
Matches 187; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 354 LPVEF-MPVPGSDSDVAAPHROPLTSSERIDKOIRYILDGISAIRKETCNKSNKNCSS 412
Db 22 LPAAPAPVPBGSDSDVAAPHROPLTSSERIDKOIRYILDGISAIRKETCNKSNKNCSS 81
QY 413 KEALAENNINLPRMAEKDCFGSGFNEETCLVKIITGLLEFEVYLEYLONRFSSSEQAR 472

Db 82 KEAALNNLNPKVAEKGGCGSGFNEETCLVITLLEFEVYLVLELQRRFSSSEQR 141
QY 473 AVQMTSTVLIQFLOKRAKNDATITPTPTNASTLITKLOAQONQWLODMTHILRSFKF 532
Db 142 AVQMTSTVLIQFLOKRAKNDATITPTPTNASTLITKLOAQONQWLODMTHILRSFKF 201
QY 533 LQSSLRALROM 543
Db 202 LQSSLRALROM 212

RESULT 29

US-08-469-318-145
Sequence 145, Application US/08469318
Patent No. 602535
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis Fusion
TITLE OF INVENTION: Protein
NUMBER OF SEQUENCES: 196
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,318
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/446,872
FILING DATE:
INFORMATION FOR SEQ ID NO: 145:
SEQUENCE CHARACTERISTICS:
LENGTH: 317 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-469-318-145

Query Match 32.7%, Score 935; DB 3; Length 317;
Best Local Similarity 63.0%; Pred. No. 2,1e-69;
Matches 206; Conservative 17; Mismatches 48; Indels 56; Gaps 7;
QY 240 DPHSNSSFYRLRELYRAERSKTFTTMMVKLOH-----HCVIDHAWSGJR 287
Db 24 DPNNLNSEDMDILMERNLRTPNLLAFVR-AVKHLENASGIEALIRNLQPLCPATAPSR 82
QY 288 HVOGLRAQEEFGCGEWS-----PEAMGTPTWT-ESSSPAENEVSTPMQALTT 336
Db 83 HPIIITKA-----GDWQEFREKLTFLVLTLEQAOBOOYIEGRISPGG----- 125
QY 337 NKDDNLIIFDSSANATSLPVEFMVPPGEDSKVAAAPHROPITSSSRIDKQIRYIIDGIS 396
Db 126 -----SGGGSNM-----APVPPGEDSKVAAAPHROPITSSSRIDKQIRYIIDGIS 170
QY 397 ALRKETCNKSNMCESSKEALAENNNLNPKVAEKGGCGSGFNEETCLVITLLEFEVY 456
Db 171 ALRKETCNKSNMCESSKEALAENNNLNPKVAEKGGCGSGFNEETCLVITLLEFEVY 230
QY 457 LEYLQNRFSSEEOAQAQVOMSTVLIQFLOKRAKNDATITPTPTNASTLITKLOAQONQW 516
Db 231 LEYLQNRFSSEEOAQAQVOMSTVLIQFLOKRAKNDATITPTPTNASTLITKLOAQONQW 290
QY 517 LQDMTHILRSFKFQSSLRALROM 543
Db 291 LQDMTHILRSFKFQSSLRALROM 317

RESULT 30
US-08-468-609A-145

Sequence 145, Application US/08468609A
Patent No. 6030812
GENERAL INFORMATION:
APPLICANT: Abrams, Mark A.
APPLICANT: Bauer, S. C.
APPLICANT: Bradford-Goldberg, Sarah R.
APPLICANT: Caparon, Maite H.
APPLICANT: Easton, Alan M.
APPLICANT: Klein, Barbara K.
APPLICANT: McKeatin, John P.
APPLICANT: Olin, Peter O.
APPLICANT: Paik, Kumman
APPLICANT: Thomas, John W.
TITLE OF INVENTION: Fusion Proteins Comprising Multiply Mutated Interleukin-3 (IL-3)
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,
ADDRESS: Corporate Patent Dept.,
STREET: P. O. Box 5110
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60680
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,609A
FILING DATE: 06-JUN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/192,325
FILING DATE: 14-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bennett, Dennis A.
REGISTRATION NUMBER: 34,547
REFERENCE/DOCKET NUMBER: C-2790/3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)737-6986
TELEFAX: (314)737-6972
INFORMATION FOR SEQ ID NO: 145:
SEQUENCE CHARACTERISTICS:
LENGTH: 317 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-468-609A-145

Query Match 32.7%, Score 935; DB 3; Length 317;
Best Local Similarity 63.0%; Pred. No. 2,1e-69;
Matches 206; Conservative 17; Mismatches 48; Indels 56; Gaps 7;
QY 240 DPHSNSSFYRLRELYRAERSKTFTTMMVKLOH-----HCVIDHAWSGJR 287
Db 24 DPNNLNSEDMDILMERNLRTPNLLAFVR-AVKHLENASGIEALIRNLQPLCPATAPSR 82
QY 288 HVOGLRAQEEFGCGEWS-----PEAMGTPTWT-ESSSPAENEVSTPMQALTT 336
Db 83 HPIIITKA-----GDWQEFREKLTFLVLTLEQAOBOOYIEGRISPGG----- 125
QY 337 NKDDNLIIFDSSANATSLPVEFMVPPGEDSKVAAAPHROPITSSSRIDKQIRYIIDGIS 396
Db 126 -----SGGGSNM-----APVPPGEDSKVAAAPHROPITSSSRIDKQIRYIIDGIS 170
QY 397 ALRKETCNKSNMCESSKEALAENNNLNPKVAEKGGCGSGFNEETCLVITLLEFEVY 456
Db 171 ALRKETCNKSNMCESSKEALAENNNLNPKVAEKGGCGSGFNEETCLVITLLEFEVY 230
QY 457 LEYLQNRFSSEEOAQAQVOMSTVLIQFLOKRAKNDATITPTPTNASTLITKLOAQONQW 516

Db 231 LEYONRFESSSEBOAAVOMSTKVLIQFLOKAKNLDATTPDPTTNASILTLQONQW 290

QY 517 LQDMTHLILRSFKEFLQSSLRALROM 543

Db 291 LQDMTHLILRSFKEFLQSSLRALROM 317

RESULT 31

US-08-446-872A-145

/ Sequence 145, Application US/08446872A

/ Patent No. 6361977

/ GENERAL INFORMATION:

/ APPLICANT: Abrams, Mark A.

/ APPLICANT: Bauer, S. C.

/ APPLICANT: Braford-Goldberg, Sarah R.

/ APPLICANT: Caparon, Maïre H.

/ APPLICANT: Easton, Alan M.

/ APPLICANT: Klein, Barbara K.

/ APPLICANT: McKearn, John P.

/ APPLICANT: Olin, Peter O.

/ APPLICANT: Paik, Kumnan

/ APPLICANT: Thomas, John W.

/ TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis

/ NUMBER OF SEQUENCES: 197

/ CORRESPONDENCE ADDRESS:

/ ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,

/ ADDRESSEE: Corporate Patent Dept.

/ STREET: P. O. Box 5110

/ CITY: Chicago

/ STATE: Illinois

/ COUNTRY: USA

/ ZIP: 60680

/ COMPUTER READABLE FORM:

/ MEDIUM TYPE: Floppy disk

/ COMPUTER: IBM PC compatible

/ OPERATING SYSTEM: PC-DOS/MS-DOS

/ SOFTWARE: Patent In Release #1.0, Version #1.25

/ CURRENT APPLICATION DATA:

/ APPLICATION NUMBER: US/08/446, 872A

/ FILING DATE: 06-JUN-1995

/ CLASSIFICATION: 424

/ PRIOR APPLICATION DATA:

/ APPLICATION NUMBER: US 08/192,325

/ FILING DATE: 14-FEB-1994

/ ATTORNEY/AGENT INFORMATION:

/ NAME: Bennett, Dennis A.

/ REGISTRATION NUMBER: 34,547

/ REFERENCE/DOCKET NUMBER: C-2790/1

/ TELECOMMUNICATION INFORMATION:

/ TELEPHONE: (314)737-6986

/ TELEFAX: (314)737-6972

/ INFORMATION FOR SEQ ID NO: 145:

/ SEQUENCE CHARACTERISTICS:

/ LENGTH: 317 amino acids

/ TYPE: amino acid

/ STRANDEDNESS:

/ TOPOLOGY: linear

/ MOLECULE TYPE: protein

/ US-08-446-872A-145

Query Match 32.7%; Score 935; DB 3; Length 317;

Best Local Similarity 63.0%; Pred. No. 2.1e-69; Indels 56; Gaps 7;

Matches 206; Conservative 17; Mismatches 48;

QY 240 DPHSWSSFYRLRFELRYAERSKPTTMMVKDLOH-----HCVIDAWSGLR 287

Db 24 DPNLNSEDMDILMERLRLPNLLAFVR-AVKHLENSGIEAIRNLQPCIPSATAPSR 82

QY 288 HAVVQLRAQSEFGGSEWMS-----PEANGTWT-ESRSPPLANEVSTPMQALTT 336

Db 83 HPIIIRK-----GDWQEFREKLTFLVLTLEQAOEQQVIEGRISPGG----- 125

QY 337 NKDDNILFRDSANATSLPEEVPVPGEDSKDVAAPHROPLTSSERIDKQIRYLDGIS 396

Db 126 -----GGGSGNM-----APVPGEDSKDVAAPHROPLTSSERIDKQIRYLDGIS 170

QY 397 AIRKETCNKSNKCESSKEALENNINLPPRAEKDGCFOGFEETLVKITGLLEFEVY 456

Db 171 ALRKETCNKSNKCESSKEALENNINLPPRAEKDGCFOGFEETLVKITGLLEFEVY 230

QY 457 LEYONRFESSSEBOAAVOMSTKVLIQFLOKAKNLDATTPDPTTNASILTLQONQW 516

Db 231 LEYONRFESSSEBOAAVOMSTKVLIQFLOKAKNLDATTPDPTTNASILTLQONQW 290

QY 517 LQDMTHLILRSFKEFLQSSLRALROM 543

Db 291 LQDMTHLILRSFKEFLQSSLRALROM 317

RESULT 32

US-08-762-227A-145

/ Sequence 145, Application US/08762227A

/ Patent No. 6436387

/ GENERAL INFORMATION:

/ APPLICANT: Abrams, Mark A.

/ APPLICANT: Bauer, S. C.

/ APPLICANT: Braford-Goldberg, Sarah R.

/ APPLICANT: Caparon, Maïre H.

/ APPLICANT: Easton, Alan M.

/ APPLICANT: Klein, Barbara K.

/ APPLICANT: McKearn, John P.

/ APPLICANT: Olin, Peter O.

/ APPLICANT: Paik, Kumnan

/ APPLICANT: Thomas, John W.

/ TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis

/ NUMBER OF SEQUENCES: 197

/ CORRESPONDENCE ADDRESS:

/ ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,

/ ADDRESSEE: Corporate Patent Dept.

/ STREET: P. O. Box 5110

/ CITY: Chicago

/ STATE: Illinois

/ COUNTRY: USA

/ ZIP: 60680

/ COMPUTER READABLE FORM:

/ MEDIUM TYPE: Floppy disk

/ COMPUTER: IBM PC compatible

/ OPERATING SYSTEM: PC-DOS/MS-DOS

/ SOFTWARE: Patent In Release #1.0, Version #1.25

/ CURRENT APPLICATION DATA:

/ APPLICATION NUMBER: US/08/762,227A

/ FILING DATE: 09-DEC-1996

/ CLASSIFICATION: <Unknown>

/ PRIOR APPLICATION DATA:

/ APPLICATION NUMBER: US 08/192,325

/ FILING DATE: 14-FEB-1994

/ APPLICATION NUMBER: US 08/446, 872

/ FILING DATE: 06-JUN-1995

/ ATTORNEY/AGENT INFORMATION:

/ NAME: Bennett, Dennis A.

/ REGISTRATION NUMBER: 34,547

/ REFERENCE/DOCKET NUMBER: C-2790/5

/ TELECOMMUNICATION INFORMATION:

/ TELEPHONE: (708) 470-6501

/ TELEFAX: (708) 470-6881

/ INFORMATION FOR SEQ ID NO: 145:

/ SEQUENCE CHARACTERISTICS:

/ LENGTH: 317 amino acids

/ TYPE: amino acid

/ STRANDEDNESS: <Unknown>

/ TOPOLOGY: linear

/ MOLECULE TYPE: protein

/ SEQUENCE DESCRIPTION: SEQ ID NO: 145:

US-08-762-227A-145

Query Match 32.7%; Score 935; DB 4; Length 317;
 Best Local Similarity 63.0%; Pred. No. 2.1e-69;
 Matches 206; Conservative 17; Mismatches 48; Indels 56; Gaps 7;

QY 240 DPHSNSSFYRLRFLRYRAERSKFTTMYVYKLOH-----HCYIHDAWSGLR 287
 |:::|
 DB 24 DPNNINSDDMDILMERNLRTPNLAFVR-AVXHLNNAAGTIALIRNLQPCLPATNAAPSR 82
 |:::|
 QY 288 HVOVLRAGEFGQGGKMSWS-----PEAMGTPT-ESRBPANENVTWQALTT 336
 |:::|
 DB 83 HPIITKA-----GDMQFFREKLTFTVLTLEQAEQOQVYIEGRISPGG-----125
 |:::|

QY 337 NKDDNLIIFRDSANATSLPVEFMVPPGEDSKDVAAAPHROPILTSSERIDKQIRYILDGIS 396
 |:::|
 DB 126 -----SGGGSNM-----APVPPGEDSKDVAAAPHROPILTSSERIDKQIRYILDGIS 170
 |:::|

QY 397 ALRKETCNKSNMCESSKEALAEENNINLPKMAEKDGGFOSGFNEETCLVKIITGLLEFEVY 456
 |:::|
 DB 171 ALRKETCNKSNMCESSKEALAEENNINLPKMAEKDGGFOSGFNEETCLVKIITGLLEFEVY 230
 |:::|

QY 457 LEYLONFESSEBOARAVOMSTKVLIQFLOKAKNLDATTPDPTNASTLTTLQAOQOW 516
 |:::|
 DB 231 LEYLONFESSEBOARAVOMSTKVLIQFLOKAKNLDATTPDPTNASTLTTLQAOQOW 290
 |:::|

QY 517 LQDMTHLILRSFKEFLQSSLRALROM 543
 |:::|
 DB 291 LQDMTHLILRSFKEFLQSSLRALROM 317
 |:::|

RESULT 33
 PCT-US95-01185-145
 / Sequence 145, Application PC/TUS9501185
 / GENERAL INFORMATION:
 / APPLICANT:
 / TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis Fusion
 / TITLE OF INVENTION: Protein
 / NUMBER OF SEQUENCES: 196
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: PCT/US95/01185
 / FILING DATE: 02-FEB-1995
 / CLASSIFICATION:
 / PRIORITY APPLICATION DATA:
 / APPLICATION NUMBER: US 08/192325
 / FILING DATE: 14-FEB-1994
 / INFORMATION FOR SEQ ID NO: 145:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 317 amino acids
 / TYPE: amino acid
 / STRANDEDNESS:
 / TOPOLOGY: linear
 / MOLECULE TYPE: protein
 / PCT-US95-01185-145

Query Match 32.7%; Score 935; DB 5; Length 317;
 Best Local Similarity 63.0%; Pred. No. 2.1e-69;
 Matches 206; Conservative 17; Mismatches 48; Indels 56; Gaps 7;

QY 240 DPHSNSSFYRLRFLRYRAERSKFTTMYVYKLOH-----HCYIHDAWSGLR 287
 |:::|
 DB 24 DPNNINSDDMDILMERNLRTPNLAFVR-AVXHLNNAAGTIALIRNLQPCLPATNAAPSR 82
 |:::|
 QY 288 HVOVLRAGEFGQGGKMSWS-----PEAMGTPT-ESRBPANENVTWQALTT 336
 |:::|
 DB 83 HPIITKA-----GDMQFFREKLTFTVLTLEQAEQOQVYIEGRISPGG-----125
 |:::|

QY 337 NKDDNLIIFRDSANATSLPVEFMVPPGEDSKDVAAAPHROPILTSSERIDKQIRYILDGIS 396
 |:::|
 DB 126 -----SGGGSNM-----APVPPGEDSKDVAAAPHROPILTSSERIDKQIRYILDGIS 170
 |:::|

QY 397 ALRKETCNKSNMCESSKEALAEENNINLPKMAEKDGGFOSGFNEETCLVKIITGLLEFEVY 456
 |:::|
 DB 171 ALRKETCNKSNMCESSKEALAEENNINLPKMAEKDGGFOSGFNEETCLVKIITGLLEFEVY 230
 |:::|

QY 457 LEYLONFESSEBOARAVOMSTKVLIQFLOKAKNLDATTPDPTNASTLTTLQAOQOW 516
 |:::|
 DB 231 LEYLONFESSEBOARAVOMSTKVLIQFLOKAKNLDATTPDPTNASTLTTLQAOQOW 290
 |:::|

QY 517 LQDMTHLILRSFKEFLQSSLRALROM 543
 |:::|
 DB 291 LQDMTHLILRSFKEFLQSSLRALROM 317
 |:::|

DB 126 -----SGGGSNM-----APVPPGEDSKDVAAAPHROPILTSSERIDKQIRYILDGIS 170
 |:::|

QY 397 ALRKETCNKSNMCESSKEALAEENNINLPKMAEKDGGFOSGFNEETCLVKIITGLLEFEVY 456
 |:::|

DB 171 ALRKETCNKSNMCESSKEALAEENNINLPKMAEKDGGFOSGFNEETCLVKIITGLLEFEVY 230
 |:::|

QY 457 LEYLONFESSEBOARAVOMSTKVLIQFLOKAKNLDATTPDPTNASTLTTLQAOQOW 516
 |:::|

DB 231 LEYLONFESSEBOARAVOMSTKVLIQFLOKAKNLDATTPDPTNASTLTTLQAOQOW 290
 |:::|

QY 517 LQDMTHLILRSFKEFLQSSLRALROM 543
 |:::|

DB 291 LQDMTHLILRSFKEFLQSSLRALROM 317
 |:::|

RESULT 34
 US-08-567-047-2
 / Sequence 2, Application US/08567047
 / Patent No. 5789552
 / Patent No. 5789552 5789555
 / GENERAL INFORMATION:
 / APPLICANT: SAVINO, Rocco
 / APPLICANT: LAHM, Armin
 / APPLICANT: CILIBERTO, Gennaro
 / TITLE OF INVENTION: METHOD FOR SELECTING SUPERAGONISTS,
 / TITLE OF INVENTION: ANTAGONISTS AND SUPRANAGONISTS FOR HORMONES HAVING
 / TITLE OF INVENTION: GP 130 AS PART OF THEIR RECEPTOR COMPLEX
 / NUMBER OF SEQUENCES: 15
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: BROWDY AND NEIMARK
 / STREET: 419 Seventh Street, N.W., Suite 300
 / City: Washington
 / STATE: D.C.
 / COUNTRY: USA
 / ZIP: 20004
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: Patent in Release #1.0, Version #1.30
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/567,047
 / FILING DATE: 04-DEC-1995
 / CLASSIFICATION: 530
 / PRIORITY APPLICATION DATA:
 / APPLICATION NUMBER: US 08/387,924
 / FILING DATE: 23-FEB-1995
 / APPLICATION NUMBER: IT RM93A000409
 / FILING DATE: 23-JUN-1993
 / ATTORNEY/AGENT INFORMATION:
 / NAME: BROWDY, Roger L.
 / REGISTRATION NUMBER: 25,618
 / REFERENCE/DOCKET NUMBER: SAVINO=1
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: 202-628-5197
 / TELEFAX: 202-737-3528
 / TELEX: 248633
 / INFORMATION FOR SEQ ID NO: 2:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 184 amino acids
 / TYPE: amino acid
 / TOPOLOGY: linear
 / MOLECULE TYPE: protein
 / US-08-567-047-2

Query Match 32.6%; Score 934; DB 1; Length 184;
 Best Local Similarity 100.0%; Pred. No. 1.1e-69;
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 360 PVPPEDESKDVAAAPHROPILTSSERIDKQIRYILDGISALRKETCNKSNMCESSKEALAE 419
 |:::|
 DB 1 PVPPEDESKDVAAAPHROPILTSSERIDKQIRYILDGISALRKETCNKSNMCESSKEALAE 60
 |:::|

QY 420 NNLPRKAEKDCGFGSGFNEETCLVKIITGLLEFEVYLEYLQNRPFSSSEQARAQVOMSTK 479
DB 61 NNLPRKAEKDCGFGSGFNEETCLVKIITGLLEFEVYLEYLQNRPFSSSEQARAQVOMSTK 120
QY 480 VLIQFLOKAKNLDATITPDPTTNASLTKLQANQWLODMTHLLRSFKEFLQSSLR 539
DB 121 VLIQFLOKAKNLDATITPDPTTNASLTKLQANQWLODMTHLLRSFKEFLQSSLR 180
QY 540 LRQM 543
DB 181 LRQM 184

RESULT 35

US-08-567-048-2
Sequence 2, Application US/08567048
Patent No. 5891998
GENERAL INFORMATION:
APPLICANT: SAVINO, Rocco
APPLICANT: LAHM, Armin
APPLICANT: CLIBERTO, Gennaro
TITLE OF INVENTION: METHOD FOR SELECTING SUPERAGONISTS,
TITLE OF INVENTION: ANTAGONISTS AND SUPERANTAGONISTS FOR HORMONES HAVING
TITLE OF INVENTION: GP 130 AS PART OF THEIR RECEPTOR COMPLEX
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/567,048
FILING DATE: 04-DEC-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/387,924
FILING DATE: 23-FEB-1995
APPLICATION NUMBER: IT RM93A000409
FILING DATE: 23-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: SAVINO=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 184 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-567-048-2

Query Match 32.6%; Score 934; DB 2; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.1e-69;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 360 PVPBGDSKQVAPHRQPLTSSRIDKQIRYILDGIALRKETCNKSNMCESSKEALAE 419
DB 1 PVPBGDSKQVAPHRQPLTSSRIDKQIRYILDGIALRKETCNKSNMCESSKEALAE 60
QY 420 NNLPRKAEKDCGFGSGFNEETCLVKIITGLLEFEVYLEYLQNRPFSSSEQARAQVOMSTK 479
DB 61 NNLPRKAEKDCGFGSGFNEETCLVKIITGLLEFEVYLEYLQNRPFSSSEQARAQVOMSTK 120

QY 480 VLIQFLOKAKNLDATITPDPTTNASLTKLQANQWLODMTHLLRSFKEFLQSSLR 539
DB 121 VLIQFLOKAKNLDATITPDPTTNASLTKLQANQWLODMTHLLRSFKEFLQSSLR 180
QY 540 LRQM 543
DB 181 LRQM 184

RESULT 36

5186931-1
Patent No. 5186931
APPLICANT: Kishimoto, Tadamiatsu; Hirano, Toshio; Akiyama, Yukio;
APPLICANT: Akira; Matsui, Hiroshi; Takahara, Yoshiyuki
TITLE OF INVENTION: COMPOSITION AND METHOD FOR SUPPORTING BONE
MARROW TRANSPLANTATION
NUMBER OF SEQUENCES: 2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/366,866
FILING DATE: 15-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 81,746
FILING DATE: 05-AUG-1987
SEQ ID NO: 1:
LENGTH: 184
5186931-1

Query Match 32.6%; Score 934; DB 6; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.1e-69;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 360 PVPBGDSKQVAPHRQPLTSSRIDKQIRYILDGIALRKETCNKSNMCESSKEALAE 419
DB 1 PVPBGDSKQVAPHRQPLTSSRIDKQIRYILDGIALRKETCNKSNMCESSKEALAE 60
QY 420 NNLPRKAEKDCGFGSGFNEETCLVKIITGLLEFEVYLEYLQNRPFSSSEQARAQVOMSTK 479
DB 61 NNLPRKAEKDCGFGSGFNEETCLVKIITGLLEFEVYLEYLQNRPFSSSEQARAQVOMSTK 120
QY 480 VLIQFLOKAKNLDATITPDPTTNASLTKLQANQWLODMTHLLRSFKEFLQSSLR 539
DB 121 VLIQFLOKAKNLDATITPDPTTNASLTKLQANQWLODMTHLLRSFKEFLQSSLR 180
QY 540 LRQM 543
DB 181 LRQM 184

RESULT 37

US-07-632-070B-1
Sequence 1, Application US/07632070B
Patent No. 5264209
GENERAL INFORMATION:
APPLICANT: Mikayama, Toshinumi
APPLICANT: Appikawa, Kadoya, Toshiniko
APPLICANT: Appikawa, Kakitani, Makoto
APPLICANT: Appikawa, Inoue, Hideo
TITLE OF INVENTION: Modified htl-6
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein,
STREET: 20 South Clark Street, Suite 2100
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
OPERATING SYSTEM: MS-DOS
SOFTWARE: NBI

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/632,070B
FILING DATE: 19901221
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-32273
FILING DATE: 13 FEB 1990
APPLICATION NUMBER: JP 2-222353
FILING DATE: 22 AUG 90
APPLICATION NUMBER: JP 2-250460
FILING DATE: 21 SEPT 1990
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 185
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: Linear
US-07-632-070B-1

Query Match 32.6%; Score 934; DB 1; Length 185;
Best Local Similarity 100.0%; Pred. No. 1,1e-69;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 360 PVPPEDESKDVAAPHROPLTSSERIDKQIRYILIDGISALRKETCNKSNMCESSKEALAE 419
DB 2 PVPPEDESKDVAAPHROPLTSSERIDKQIRYILIDGISALRKETCNKSNMCESSKEALAE 61
QY 420 NLNLPKRAEKDGCFOGFEETCLVKIITGLFEFVYLEYONRFESSSEQARAVOMSTK 479
DB 62 NLNLPKRAEKDGCFOGFEETCLVKIITGLFEFVYLEYONRFESSSEQARAVOMSTK 121
QY 480 VLIOFLQKAKNLDATTPDPTTNASLITKLOAQONQWLODMTHLILRSFKEFLQSSIRA 539
DB 122 VLIOFLQKAKNLDATTPDPTTNASLITKLOAQONQWLODMTHLILRSFKEFLQSSIRA 181
QY 540 LRQM 543
DB 182 LRQM 185

RESULT 38
US-07-918-181A-2
Sequence 2, Application US/07918181A
Patent No. 5338833
GENERAL INFORMATION:
APPLICANT: Fowles, Dana M.
TITLE OF INVENTION: C-Terminal IL-6 Muteins
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Imclone Systems Incorporated
STREET: 180 Varick Street
CITY: New York
STATE: New York
COUNTRY: United States
ZIP: 10014
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/918,181A
FILING DATE: 23-JUL-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sheets, Eric J.
REGISTRATION NUMBER: 30,326
REFERENCE/DOCKET NUMBER: FOW-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:

LENGTH: 185 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-918-181A-2

Query Match 32.6%; Score 934; DB 1; Length 185;
Best Local Similarity 100.0%; Pred. No. 1,1e-69;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 360 PVPPEDESKDVAAPHROPLTSSERIDKQIRYILIDGISALRKETCNKSNMCESSKEALAE 419
DB 2 PVPPEDESKDVAAPHROPLTSSERIDKQIRYILIDGISALRKETCNKSNMCESSKEALAE 61
QY 420 NLNLPKRAEKDGCFOGFEETCLVKIITGLFEFVYLEYONRFESSSEQARAVOMSTK 479
DB 62 NLNLPKRAEKDGCFOGFEETCLVKIITGLFEFVYLEYONRFESSSEQARAVOMSTK 121
QY 480 VLIOFLQKAKNLDATTPDPTTNASLITKLOAQONQWLODMTHLILRSFKEFLQSSIRA 539
DB 122 VLIOFLQKAKNLDATTPDPTTNASLITKLOAQONQWLODMTHLILRSFKEFLQSSIRA 181
QY 540 LRQM 543
DB 182 LRQM 185

RESULT 39
US-08-231-575-2
Sequence 2, Application US/08231575
Patent No. 5565336
GENERAL INFORMATION:
APPLICANT: Fowles, Dana M.
TITLE OF INVENTION: C-Terminal IL-6 Muteins
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Imclone Systems Incorporated
STREET: 180 Varick Street
CITY: New York
STATE: New York
COUNTRY: United States
ZIP: 10014
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/231,575
FILING DATE: 22-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sheets, Eric J.
REGISTRATION NUMBER: 30,326
REFERENCE/DOCKET NUMBER: FOW-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 185 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-231-575-2

Query Match 32.6%; Score 934; DB 1; Length 185;
Best Local Similarity 100.0%; Pred. No. 1,1e-69;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 360 PVPGEDSKDVAAPHROPLTSSERIDKQIRYIIDGISALRKETCNKNMCESSKEALAEN 419
DB 2 PVPGEDSKDVAAPHROPLTSSERIDKQIRYIIDGISALRKETCNKNMCESSKEALAEN 61
QY 420 NINLPMAEKDCGFGSGFNEETCLVKIITGLLEFEVYLEYLONRPFSSSEQARAAYOMSTK 479
DB 62 NINLPMAEKDCGFGSGFNEETCLVKIITGLLEFEVYLEYLONRPFSSSEQARAAYOMSTK 121
QY 480 VLIQFLOKKAQKLDATITPPDPTTNASLTKLOAONQWLODMTHLILRSFKFELQSSLRA 539
DB 122 VLIQFLOKKAQKLDATITPPDPTTNASLTKLOAONQWLODMTHLILRSFKFELQSSLRA 181
QY 540 LRQM 543
DB 182 LRQM 185

RESULT 40

US-08-246-427A-5
; Sequence 5, Application US/08246427A
; Patent No. 5641657
; GENERAL INFORMATION:
; APPLICANT: ROSEN, ET AL.
; TITLE OF INVENTION: Interleukin-6 Splice Variant
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/246,427A
; FILING DATE: Submitted herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/246,427
; FILING DATE: MAY 19, 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 185 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
; US-08-246-427A-5

Query Match 32.6%; Score 934; DB 1; Length 185;
Best Local Similarity 100.0%; Pred. No. 1.1e-69;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 360 PVPGEDSKDVAAPHROPLTSSERIDKQIRYIIDGISALRKETCNKNMCESSKEALAEN 419
DB 2 PVPGEDSKDVAAPHROPLTSSERIDKQIRYIIDGISALRKETCNKNMCESSKEALAEN 61
QY 420 NINLPMAEKDCGFGSGFNEETCLVKIITGLLEFEVYLEYLONRPFSSSEQARAAYOMSTK 479
DB 62 NINLPMAEKDCGFGSGFNEETCLVKIITGLLEFEVYLEYLONRPFSSSEQARAAYOMSTK 121

QY 480 VLIQFLOKKAQKLDATITPPDPTTNASLTKLOAONQWLODMTHLILRSFKFELQSSLRA 539
DB 122 VLIQFLOKKAQKLDATITPPDPTTNASLTKLOAONQWLODMTHLILRSFKFELQSSLRA 181
QY 540 LRQM 543
DB 182 LRQM 185

Search completed: December 9, 2004, 09:22:48
Job time: 56.714 secs

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OM protein - protein search, using sw model

Run on: December 9, 2004, 08:39:26 / Search time 210.95 Seconds
(without alignments)
923.396 Million cell updates/sec

Title: US-09-462-416-7

Perfect score: 2861

Sequence: 1 MAAVGCALALAAVGNAL.....LILRSFKPLQSLRALRQM 543

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_23sep04:*
1: geneseqp1980s:*
2: geneseqp1980s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2861	100.0	543	2	AAV03164
2	2769.5	96.8	570	6	ABP72702
3	2663.5	93.1	515	3	AAAB5404
4	2646	92.5	525	2	AAW36846
5	2512.5	87.8	500	2	AAW36847
6	2149.5	75.1	419	2	AAV30938
7	1921	67.1	592	2	AAW70797
8	1921	67.1	592	3	AAV92185
9	1921	67.1	592	7	ABW02165
10	1918	67.0	468	1	AAV90284
11	1918	67.0	468	2	AAAR37215
12	1918	67.0	468	4	AAAB3655
13	1918	67.0	468	5	AAE28593
14	1918	67.0	468	5	ABW78191
15	1918	67.0	468	5	ABP72697
16	1918	67.0	468	7	ABW72697
17	1917	67.0	690	3	AAV92195
18	1915.5	67.0	468	3	AAV92196
19	1915	66.9	468	2	AAAB3654
20	1913	66.9	357	6	ABP72699
21	1912	66.8	477	2	AAV92197
22	1910	66.8	360	2	AAW70804
23	1910	66.8	360	3	AAV92199
24	1910	66.8	360	7	ABW02172
25	1910	66.8	468	1	AAV90525

26	1907	66.7	364	6	ABP72698	Abp72698 Soluble i
27	1900	66.4	468	2	AAW71371	AAW71371 Human int
28	1858	64.9	345	3	AAV55071	AAV55071 SR345 pro
29	1852	64.7	344	1	AAV90528	AAV90528 B cell bc
30	1788	62.5	1158	3	AAV92205	AAV92205 Fusion po
31	1788	62.5	1158	7	ABW02178	ABW02178 Human cyt
32	1783	62.3	1168	3	AAV92204	AAV92204 Fusion po
33	1783	62.3	1168	7	ABW02177	ABW02177 Human cyt
34	1763	61.6	325	7	AAO23014	AAO23014 Human int
35	1759	61.5	1042	2	AAV70122	AAV70122 IL8-R typ
36	1757	61.4	325	2	AAO23016	AAO23016 Human int
37	1754	61.3	325	7	AAO23018	AAO23018 Human int
38	1748	61.1	325	3	AAV15389	AAV15389 Human int
39	1748	61.1	325	3	AAV15390	AAV15390 Bovine in
40	1748	61.1	325	7	AAO23015	AAO23015 Human int
41	1742	60.9	325	7	AAO23017	AAO23017 Human int
42	1715	59.9	323	1	AAV90527	AAV90527 B cell bc
43	1683	58.8	315	2	AAW70805	AAW70805 Amino ac1
44	1683	58.8	315	3	AAV92200	AAV92200 Soluble h
45	1683	58.8	315	7	ABW02173	ABW02173 Human IL-

ALIGNMENTS

RESULT 1
ID AAY03164 standard; protein; 543 AA.
XX
AC AAY03164;
XX
DT 11-JUN-1999 (first entry)
XX
DE Chimeric sIL-6R/IL-6 protein.
XX
XX Soluble interleukin-6 receptor; interleukin-6; sIL-6; IL-6; IL-6/IL-6;
KW chimeric protein; fusion protein; cell growth inhibitor; melanoma cell;
KW highly malignant cancer cell; in vivo engraftment; mammalian cancer;
KW human hematopoietic cell; bone marrow transplantation; mammalian cancer;
KW hepatotoxic agent protection; hematopoiesis; liver disorder;
KW neurological disorder.
XX
OS Synthetic.
XX
PN WO9902552-A2.
XX
PD 21-JAN-1999.
XX
PF 09-JUL-1998; 98WO-IL000321.
XX
PR 10-JUL-1997; 97IL-00121284.
PR 30-DEC-1997; 97IL-00122818.
XX
PA (YEDA) YEDA RES & DEV CO LTD.
XX
PI Revel M, Chebath J, Lapidot T, Kollet O;
XX
XX WPI, 1999-120776/10.
XX
XX New glycosylated soluble IL-6 receptor/IL-6 conjugates - used for e.g.
PT treating cancers, bone marrow transplantation, increasing hematopoiesis
PT or treating liver or neurological disorders.
XX
PS Claim 6; Fig 3; 77bp; English.
XX
XX This sequence represents the chimeric glycosylated soluble interleukin-6
CC receptor (sIL-6R)-interleukin-6 (IL-6) protein (sIL-6R/IL-6) of the
CC invention. It comprises a fusion protein product between all of the
CC naturally occurring form of sIL-6R and all of the naturally occurring
CC form of IL-6, the sIL-6/IL-6 and analogues being glycosylated in a
CC similar fashion to the glycosylation of naturally occurring sIL-6R and IL
CC -6. The sIL-6R/IL-6 and analogues are capable of inhibiting the growth of
CC highly malignant cancer cells, e.g. melanoma cells, eliciting the in vivo

CC engraftment of human haematopoietic cells in bone marrow transplantation
 CC and protecting liver from hepatotoxic agents. They can be used for the
 CC preparation of a medicament for treating mammalian cancers by way of
 CC inhibition of cancer cells, for enhancement of bone marrow
 CC transplantation by way of eliciting engraftment of human haematopoietic
 CC cells in bone marrow transplantation, for increasing haematopoiesis, for
 CC treating liver or neurological disorders, or in other applications in
 CC which IL-6 or sIL-6R are used

XX Sequence 543 AA;

Query Match 100.0%; Score 2861; DB 2; Length 543;
 Best Local Similarity 100.0%; Pred. No. 4.2e-183;
 Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNAVGCALIAALIAAPGALAPRRCPAOGVAVRGVLTSLPGDSVTLTTCPGVPEEDNATVHW 60
 DB 1 MNAVGCALIAALIAAPGALAPRRCPAOGVAVRGVLTSLPGDSVTLTTCPGVPEEDNATVHW 60
 QY 61 VLKRPAGSHPSRMWGMGRLLRSVOLHDSGNYSCYRAGRPAQTVHLLVDVPEEPQLS 120
 DB 61 VLKRPAGSHPSRMWGMGRLLRSVOLHDSGNYSCYRAGRPAQTVHLLVDVPEEPQLS 120
 QY 121 CFRKSPISNVVCEWGPSTPSLTTRKAVILVRKFQNSPAEDPQEPQYQSQESQKFSQCLAV 180
 DB 121 CFRKSPISNVVCEWGPSTPSLTTRKAVILVRKFQNSPAEDPQEPQYQSQESQKFSQCLAV 180
 QY 181 PEGDSSFYIVSMCVASSVSGSKFTQTFQCGIILQPPPANITVTVAARNPRMLSVTWQ 240
 DB 181 PEGDSSFYIVSMCVASSVSGSKFTQTFQCGIILQPPPANITVTVAARNPRMLSVTWQ 240
 QY 241 PHSNSSFYLRPELRYARSRKSTFTTWYKDLQHHCVIHDAMSGLRHVQLRAQEEFGQ 300
 DB 241 PHSNSSFYLRPELRYARSRKSTFTTWYKDLQHHCVIHDAMSGLRHVQLRAQEEFGQ 300
 QY 301 GEMSEMPAMGTWTSRSRPPANEVSTWQALTTNKDDNIIFRDSANATSLPVEFMP 360
 DB 301 GEMSEMPAMGTWTSRSRPPANEVSTWQALTTNKDDNIIFRDSANATSLPVEFMP 360
 QY 361 VPPGEDSKDVAAPRROPULTSERIDKQIRYILDGISALRKETCKSKMCKSSKEALENN 420
 DB 361 VPPGEDSKDVAAPRROPULTSERIDKQIRYILDGISALRKETCKSKMCKSSKEALENN 420
 QY 421 LNP.PKMAEKDGCFOSGFNEBCTVKIITGLLEFEVYLEYLONPESSEBQARAQVOMSTKV 480
 DB 421 LNP.PKMAEKDGCFOSGFNEBCTVKIITGLLEFEVYLEYLONPESSEBQARAQVOMSTKV 480
 QY 481 LIQFLQKKAKNLDALITTPDTTNAASLITKLOAQONQIQLDMTTHILRSFKEFIQSSIRAL 540
 DB 481 LIQFLQKKAKNLDALITTPDTTNAASLITKLOAQONQIQLDMTTHILRSFKEFIQSSIRAL 540
 QY 541 ROM 543
 DB 541 ROM 543

RESULT 2
 ABP72702
 ID ABP72702 standard; protein; 570 AA.
 AC ABP72702;
 XX

DT 11-JUN-2003 (first entry)

DE Human interleukin-6-receptor isoform DS-sIL-6R fusion protein.

KW Human; interleukin-6; receptor; DS-sIL-6R; antibacterial; virucide;

KM anti-HIV; antineumatic; antiarthritic; antiinflammatory;

XX immunosuppressive; gene therapy.

OS Homo sapiens.

OS Synthetic.

OS Chimeric.

XX Key Location/Qualifiers
 FH Protein 1..364 DS-sIL-6R
 FT Peptide /label=.376
 FT Protein /label=Linker
 FT Peptide /label=IL-6
 FT Peptide /label=.570
 FT Peptide /label=C-myc tag

PN WO2003014359-A2.

XX 20-FEB-2003.

PF 02-AUG-2002; 2002WO-GB003581.

XX 03-AUG-2001; 2001GB-00019015.

PA (UYCA-) UNIV COLLEGE CARDIFF.
 (UYMA-) UNIV WALES COLLEGE OF MEDICINE.

XX Jones SA, Topley N;

XX WPI; 2003-256588/25.

PT New fusion protein having a functional IL-6 and DS-sIL-6R molecule,
 PT useful for the manufacture of a medicament for the prophylaxis or
 PT treatment of an infectious disease, and an inflammatory or immunological
 PT disorder.

XX Disclosure; Fig 5; 46pp; English.

CC The present sequence is the protein sequence of a novel fusion protein
 CC comprising a soluble form of the human interleukin-6 receptor, denoted DS
 CC sIL-6R (see also ABP72698), joined via a peptide linker to a human IL-6
 CC molecule (see also ABP72700), with a C-terminal c-myc tag sequence.
 CC Administration of this fusion protein results in the increased expression
 CC of one or more of MIP-1alpha, MIP-1beta, RANTES or IP-10. High levels of
 CC MIP-1alpha, MIP-1beta and RANTES complete with HIV for binding to CCR5
 CC and effectively suppress HIV entry. The fusion protein can be used in the
 CC treatment of any disease in which the infectious agent binds to CCR5,
 CC especially M-trophic strains of HIV. The invention also provides a
 CC nucleic acid molecule encoding the fusion protein, an expression vector,
 CC a host cell, and a method of producing the fusion protein in the host
 CC cell. The fusion protein, nucleic acid or vector can be used in the
 CC manufacture of a medicament for the prophylaxis or treatment of an
 CC infectious disease (especially AIDS caused by a M-trophic strain of HIV,
 CC or bacterial peritonitis), an inflammatory disorder or an immunological
 CC disorder (especially rheumatoid arthritis), when it is desirable to
 CC increase or resolve an immune response (claimed)

XX Sequence 570 AA;

Query Match 96.8%; Score 2769.5; DB 6; Length 570;
 Best Local Similarity 95.4%; Pred. No. 6e-177;
 Matches 536; Conservative 0; Mismatches 5; Indels 21; Gaps 4;

QY 1 MNAVGCALIAALIAAPGALAPRRCPAOGVAVRGVLTSLPGDSVTLTTCPGVPEEDNATVHW 60
 DB 1 MNAVGCALIAALIAAPGALAPRRCPAOGVAVRGVLTSLPGDSVTLTTCPGVPEEDNATVHW 60
 QY 61 VLKRPAGSHPSRMWGMGRLLRSVOLHDSGNYSCYRAGRPAQTVHLLVDVPEEPQLS 120
 DB 61 VLKRPAGSHPSRMWGMGRLLRSVOLHDSGNYSCYRAGRPAQTVHLLVDVPEEPQLS 120
 QY 121 CFRKSPISNVVCEWGPSTPSLTTRKAVILVRKFQNSPAEDPQEPQYQSQESQKFSQCLAV 179
 DB 121 CFRKSPISNVVCEWGPSTPSLTTRKAVILVRKFQNSPAEDPQEPQYQSQESQKFSQCLAV 179
 QY 180 PEGDSSFYIVSMCVASSVSGSKFTQTFQCGIILQPPPANITVTVAARNPRMLSVTWQ 239
 DB 180 PEGDSSFYIVSMCVASSVSGSKFTQTFQCGIILQPPPANITVTVAARNPRMLSVTWQ 238

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QY 240 DPHSNMSFFRYRLRFEFLRYRAERSKTFETTMVVKDLOHHCVIHDAMSGLRHVOLRAQEEFG 299
DB 239 DPHSNMSFFRYRLRFEFLRYRAERSKTFETTMVVKDLOHHCVIHDAMSGLRHVOLRAQEEFG 298
QY 300 QGEMSWMSPEAMGTPWTESSRSPPAENEVSTPMQALTTNKDDNLLFRDSANATSLP---- 355
DB 299 QGEMSWMSPEAMGTPWTESSRSPPAENEVSTPMQALTTNKDDNLLFRDSANATSLP----- 358
QY 356 -----VEFMVPPPEGDSKDVAAHPHROPULTSSERIDKQIRYILDDISALRKE 401
DB 359 RSCSGIGGGGGGGGGLBEPVPEGDSKDVAAHPHROPULTSSERIDKQIRYILDDISALRKE 418
QY 402 TCNKSNNMCESSKEALAEENNLLPJKMAEKDGCFOGSGNEETCLVKIITGLLEFEVLEYIQ 461
DB 419 TCNKSNNMCESSKEALAEENNLLPJKMAEKDGCFOGSGNEETCLVKIITGLLEFEVLEYIQ 478
QY 462 NPFESSEEQARAVOMSTKVLIOFLQKAKNLDALITPPPTTNASLLTKLQAOQWLODMT 521
DB 479 NPFESSEEQARAVOMSTKVLIOFLQKAKNLDALITPPPTTNASLLTKLQAOQWLODMT 538
QY 522 THILRSFKFLOSSLRALRQM 543
DB 539 THILRSFKFLOSSLRALRQM 560

RESULT 3
AAB15404
ID AAB15404 standard; protein; 515 AA.
AC AAB15404;
XX
XX 17-JAN-2001 (first entry)
DE IL-6R/IL-6 fusion protein.
XX
XX Fusion protein; human; interleukin 6 receptor; Pichia pastoris; yeast;
KM drug; myeloid stem cell; platelet; blood.
XX
OS Homo sapiens.
OS Synthetic.
FH Key Location/Qualifiers
FT Misc-difference 57 /note= "encoded by GGC"
FT Misc-difference 281 /note= "encoded by CAA"
FT Misc-difference /note= "encoded by CAA"
PN JP200016539-A.
XX
XX 20-JUN-2000.
XX
XX 03-DEC-1998; 98JP-00343933.
XX
XX 03-DEC-1998; 98JP-00343933.
XX
XX (TOYO ) TOSOH CORP.
XX
XX WPI; 2000-485548/43.
XX
XX N-PSDB; AAA70763.
XX
XX Yeast of Pichia pastoris genus transformed by expression vector
PT containing gene encoding fused protein of interleukin-6 receptor (IL-6R)
PT protein for amplifying myeloid stem cells and increasing platelets.
XX
XX Example 1; Page 8-10; 11pp; Japanese.
XX
XX The invention relates to the production of a fusion protein comprising
CC the human interleukin 6 receptor (IL-6R) fused to the human IL-6 protein
CC in a Pichia pastoris yeast cell. This sequence represents the IL-6R/IL-6
CC fusion protein. The coding sequence for this protein is cloned into an
CC expression vector for introduction into P. pastoris. The IL-6R protein is
CC used as a drug for amplifying myeloid stem cells and increasing platelets
CC

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CC in blood
XX
XX Sequence 515 AA;
SQ
Query Match 93.1%; Score 2663.5; DB 3; Length 515;
Best Local Similarity 96.8%; Pred. No. 6,6e-170;
Matches 507; Conservative 1; Mismatches 7; Indels 9; Gaps 1;

QY 20 LAPRCPAQEVARGVLTSLPGDSVTLTCGVPEDNATVHWLRLKPAAGSHSRMAGMR 79
DB 1 LAPRCPAQEVARGVLTSLPGDSVTLTCGVPEDNATVHWLRLKPAAGSHSRMAGMR 60
QY 80 RLLRSVQLHDSGNVSCYRAGRPAQTVHLLVDPPEEPOLSCFRKSPLSNVVCEMPRST 139
DB 61 RLLRSVQLHDSGNVSCYRAGRPAQTVHLLVDPPEEPOLSCFRKSPLSNVVCEMPRST 120
QY 140 PSLTTKAVLLVRKFNQNSPADPFOEPCQVSOESQKTSQCLAVPEGDSSFYIVSCVASSVG 199
DB 121 PSLTTKAVLLVRKFNQNSPADPFOEPCQVSOESQKTSQCLAVPEGDSSFYIVSCVASSVG 180
QY 200 SKFSKTQTFQGGGIIQDPDPANITVAVARNRMLSVTWQDPHSNMSFFRYRLRFEFLRYRA 259
DB 181 SKFSKTQTFQGGGIIQDPDPANITVAVARNRMLSVTWQDPHSNMSFFRYRLRFEFLRYRA 240
QY 260 ERSKTFETTMVVKDLOHHCVIHDAMSGLRHVOLRAQEEFGQEMSWMSPEAMGTPWTESSR 319
DB 241 ERSKTFETTMVVKDLOHHCVIHDAMSGLRHVOLRAQEEFGQEMSWMSPEAMGTPWTESSR 300
QY 320 SPPAENEVSTPMQALTTNKDDNLLFRDSANATSLPVEFMVPPVPEGDSKDVAAHPHROPULT 379
DB 301 SPPAENEVSTPMQALTTNKDDNLLSELY-----APVPPEGDSKDVAAHPHROPULT 351
QY 380 SSERIDKQIRYILDDISALRKECTCNKSNMCESSKEALAEENNLLPMAKEDGCFOSGNE 439
DB 352 SSERIDKQIRYILDDISALRKECTCNKSNMCESSKEALAEENNLLPMAKEDGCFOSGNE 411
QY 440 ETCVLKIIIGLLEFEVLEYLQNRPFESSEEQARAVOMSTKVLIOFLQKAKNLDALITTPD 499
DB 412 ETCVLKIIIGLLEFEVLEYLQNRPFESSEEQARAVOMSTKVLIOFLQKAKNLDALITTPD 471
QY 500 PTTNASLLTKLQAOQWLODMTTHILRSFKFLOSSLRALRQM 543
DB 472 PTTNASLLTKLQAOQWLODMTTHILRSFKFLOSSLRALRQM 515

RESULT 4
AAW36846
ID AAW36846 standard; protein; 525 AA.
AC AAW36846;
XX
XX 25-MAR-2003 (revised)
DT 25-MAR-1998 (first entry)
XX
XX Human fusion polypeptide H-IL-6 with 18 amino acid linker.
XX
XX Interleukin-6; IL-6; interleukin-6 receptor; IL-6R; ligand; conjugate;
KM protein interaction; therapeutic; antagonist.
XX
XX Synthetic.
OS Homo sapiens.
OS
OS
FH Key Location/Qualifiers
FT Peptide 1..19 /label= signal_peptide
FT Protein 20..524 /label= signal_peptide
FT Region 324..341 /note= "H-IL-6 fusion polypeptide"
FT 324..341 /label= linker region
FT /note= "links together COOH-terminus of sIL-6R with the
XX NH2-terminus of IL-6"
XX
XX MO9732891-A2.

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XX 12-SEP-1997.
 PD 07-MAR-1997; 97WO-DE000458.
 XX 07-MAR-1996; 96DE-01008813.
 XX (ANGE-) ANGEWANDTE GENTECHNOLOGIE SYSTEME GMBH.
 PA Rosejohn S;
 PI WPI: 1997-470536/43.
 DR N-PSDB; AAT97848.
 XX Conjugate of two peptide(s) with mutual affinity connected by a linker -
 PT used to modulate interactions between proteins, e.g. for ex vivo
 XX expansion of human stem cells.
 PS Disclosure; Fig 1; 19pp; German.
 XX This sequence represents the fusion polypeptide H-IL-6 which contains an
 CC 18 amino acid linker which joins the carboxy terminus of human
 CC interleukin-6 receptor (IL-6R) with the amino terminus of human
 CC interleukin-6 (IL-6). Such conjugates could be used to modulate
 CC interactions between proteins, particularly to overcome interrupted
 CC interactions caused by an incomplete interleukin-6 (IL-6) receptor. These
 CC constructs derived from IL-6 and its receptor, can also be used for ex
 CC vivo expansion of human stem cells, and as a therapeutic IL-6 receptor
 CC antagonist. (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-
 CC MAR-2003 to correct PI field.)
 XX
 SQ Sequence 525 AA;
 Query Match 92.5%; Score 2646; DB 2; Length 525;
 Best Local Similarity 93.7%; Pred. No. 1e-168;
 Matches 509; Conservative 2; Mismatches 14; Indels 18; Gaps 2;

QY 1 MLAVGCLLALALPAALAPRRCPAEOVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60
 DB 1 MLAVGCLLALALPAALAPRRCPAEOVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60
 QY 61 VLKRPAGSHPRWAGRRLLRSVQHDGNSCVRRARPGVTLVLDVPEEPQLS 120
 DB 61 VLKRPAGSHPRWAGRRLLRSVQHDGNSCVRRARPGVTLVLDVPEEPQLS 120
 QY 121 CPERKPLSNVVCWGPSTSLTTKAVLVKRFQNSPAEDFOBPCCOYSQSKFSCQIAV 180
 DB 121 CPERKPLSNVVCWGPSTSLTTKAVLVKRFQNSPAEDFOBPCCOYSQSKFSCQIAV 180
 QY 181 PEDDSSTYITSMCVASVSGSKFTQTQFCGGLLOPPPNITVTVAANPRMLSVTWOD 240
 DB 181 PEDDSSTYITSMCVASVSGSKFTQTQFCGGLLOPPPNITVTVAANPRMLSVTWOD 240
 QY 241 PHSNNSFFYLRPELRARERSKFTTMMVKDLOHCHVIDHMSGIRHVQVLAQSEFQ 300
 DB 241 PHSNNSFFYLRPELRARERSKFTTMMVKDLOHCHVIDHMSGIRHVQVLAQSEFQ 300
 QY 301 GEWSEMSPEAMGTPTWESRSPPAENEVSPTMALTTNKDDNILFRDSANATSLPVEFMP 360
 DB 301 GEWSEMSPEAMGTPTWESRSPPAENEVSPTMALTTNKDDNILFRDSANATSLPVEFMP 360
 QY 361 VPGESEKDVAAHRQPLTSSSEIDQIRIILDGISALRKETNKSNMCESSKEALAEKN 420
 DB 361 VPGESEKDVAAHRQPLTSSSEIDQIRIILDGISALRKETNKSNMCESSKEALAEKN 420
 QY 421 LNLPKAAEKDQCFQSGFNEBETCLVKIITGLLEFEVLEYLQNFESSEQARAVOMSTV 480
 DB 421 LNLPKAAEKDQCFQSGFNEBETCLVKIITGLLEFEVLEYLQNFESSEQARAVOMSTV 480
 QY 481 LLOFLQKAKNDATITPTPTNASILTYLQAOQWLODMTTHLILRSFKEFLQSSIRAL 540
 DB 481 LLOFLQKAKNDATITPTPTNASILTYLQAOQWLODMTTHLILRSFKEFLQSSIRAL 540
 QY 540 LLOFLQKAKNDATITPTPTNASILTYLQAOQWLODMTTHLILRSFKEFLQSSIRAL 540
 DB 540 LLOFLQKAKNDATITPTPTNASILTYLQAOQWLODMTTHLILRSFKEFLQSSIRAL 540

QY 541 ROM 543
 DB 523 ROM 525
 RESULT 5
 AAM36847
 ID AAM36847 standard; protein; 500 AA.
 AC AAM36847;
 XX 25-MAR-2003 (revised)
 DT 25-MAR-1998 (first entry)
 XX
 DE Human fusion polypeptide H-IL-6 with 13 amino acid linker.
 XX Interleukin-6; IL-6; interleukin-6 receptor; IL-6R; ligand; conjugate;
 KW protein interaction; therapeutic; antagonist.
 XX
 OS Synthetic.
 OS Homo sapiens.
 OS
 FH Key Location/Qualifiers
 FT Peptide 1..19
 FT /label= signal_peptide
 FT Protein 20..500
 FT /note= "H-IL-6 fusion polypeptide"
 FT Region 304..316
 FT /label= linker region
 FT /note= "Links together COOH-terminus of sIL-6R with the
 FT NH2-terminus of IL-6"
 XX
 PN MO9732891-A2.
 PD 12-SEP-1997.
 XX 07-MAR-1997; 97WO-DE000458.
 PF 07-MAR-1996; 96DE-01008813.
 PR (ANGE-) ANGEWANDTE GENTECHNOLOGIE SYSTEME GMBH.
 XX Rosejohn S;
 PI WPI: 1997-470536/43.
 DR N-PSDB; AAT97849.
 DR Conjugate of two peptide(s) with mutual affinity connected by a linker -
 PT used to modulate interactions between proteins, e.g. for ex vivo
 PT expansion of human stem cells.
 XX
 PS Disclosure; Fig 2; 19pp; German.
 XX This sequence represents the fusion polypeptide H-IL-6 which contains an
 CC 13 amino acid linker which joins the carboxy terminus of human
 CC interleukin-6 receptor (IL-6R) with the amino terminus of human
 CC interleukin-6 (IL-6). Such conjugates could be used to modulate
 CC interactions between proteins, particularly to overcome interrupted
 CC interactions caused by an incomplete interleukin-6 (IL-6) receptor. These
 CC constructs derived from IL-6 and its receptor, can also be used for ex
 CC vivo expansion of human stem cells, and as a therapeutic IL-6 receptor
 CC antagonist. (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-
 CC MAR-2003 to correct PI field.)
 XX
 SQ Sequence 500 AA;
 Query Match 87.8%; Score 2512.5; DB 2; Length 500;
 Best Local Similarity 90.1%; Pred. No. 8.3e-160;
 Matches 489; Conservative 1; Mismatches 10; Indels 43; Gaps 3;

QY 1 MLAVGCLLALALPAALAPRRCPAEOVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60
 DB 1 MLAVGCLLALALPAALAPRRCPAEOVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60


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QY 61 VLKRPAGSHPSRWAGMGRLLRLRSVOLHDSGNVSCYRAGRPAQVHLVDPPEEPQIS 120
DB 61 VLKRPAGSHPSRWAGMGRLLRLRSVOLHDSGNVSCYRAGRPAQVHLVDPPEEPQIS 120
QY 121 CRRKSPLSNVVCEWGRSTPSLTTKAVILVRKFQNSPAEDFOEPCQYSESQKFSQCLAV 180
DB 121 CRRKSPLSNVVCEWGRSTPSLTTKAVILVRKFQNSPAEDFOEPCQYSESQKFSQCLAV 180
QY 181 PGDSSFYIVSMCVASSVSGSKFTQTFQCGILQDPDPANITVTVAARNPRLSVTWGD 240
DB 181 PGDSSFYIVSMCVASSVSGSKFTQTFQCGILQDPDPANITVTVAARNPRLSVTWGD 240
QY 241 PHSNNSFYRLRFELRYRARSKTFTTMMVKDLOHHCVIDHWSGLRHVVOLRAOEFGQ 300
DB 241 PHSNNSFYRLRFELRYRARSKTFTTMMVKDLOHHCVIDHWSGLRHVVOLRAOEFGQ 280
QY 301 GEMSEWSPAMGTPWTESRSPPAENEVSTPMQALITTKDDNILFRDSANATSLPYEFMP 360
DB 301 GEMSEWSPAMGTPWTESRSPPAENEVSTPMQALITTKDDNILFRDSANATSLPYEFMP 317
QY 361 VPPGESSKVAAAPHROPULTSSERIDKQIRIYILDGISAARKETCNKSNMCESSKEALAENX 420
DB 361 VPPGESSKVAAAPHROPULTSSERIDKQIRIYILDGISAARKETCNKSNMCESSKEALAENX 377
QY 421 LNLPRKAEKDCGFCFSGFNEETCLVKIITGILEFEVYLEYIQRNRPESSEBOARAVOMSTKY 480
DB 421 LNLPRKAEKDCGFCFSGFNEETCLVKIITGILEFEVYLEYIQRNRPESSEBOARAVOMSTKY 437
QY 481 LIQFLQKKAKNLDAITTPDPTNASTLTTLQAOQOMLQDMTTHLILRSFKFLOSSLRAL 540
DB 481 LIQFLQKKAKNLDAITTPDPTNASTLTTLQAOQOMLQDMTTHLILRSFKFLOSSLRAL 497
QY 541 ROM 543
DB 541 ROM 500

RESULT 6
AA30938
ID AAY30938 standard; protein; 419 AA.
XX
AC AAY30938;
XX
DT 19-OCT-1999 (first entry)
XX
DE Human IL-6 receptor/IL-6 fusion protein.
XX
KW IL-6; interleukin-6; receptor; human; fusion protein; bone marrow;
XX
KW stem cell; platelet; reduced antigenicity.
XX
OS Homo sapiens.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Protein 1..420
FT /note="No start codon given"
FT
XX
PN JP1196867-A.
XX
PD 27-JUL-1999.
XX
PF 09-JAN-1998; 98JP-00002921.
XX
PR 09-JAN-1998; 98JP-00002921.
XX
PA (TOYO ) TOSOH CORP.
XX
DR MPI: 1999-496648/42.
XX
DR N-PSDB; AA209202.
XX
PT New interleukin-6 receptor-interleukin-6 fused protein and gene - used
PT for growth of bone marrow stem cells and platelets.

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XX
PS Example 1; Page 5-8; 8pp; Japanese.
XX.
CC This invention describes a novel gene which encodes a fusion protein of
CC interleukin-6 (IL-6) receptor and bound with a gene sequence encoding for
CC IL-6 at the downstream of IL-6 receptor gene. The gene and its encoding
CC protein has applications for the growth of bone marrow stem cells and
CC platelets. Transmission of a signal of IL-6 to target cells for
CC stimulation with reduced antigenicity is possible. This sequence
CC represents the IL-6 receptor/IL-6 fusion protein described in the
CC invention
XX
SQ Sequence 419 AA;
XX
Query Match 75.1%; Score 2149.5; DB 2; Length 419;
Best Local Similarity 95.8%; Pred. No. 1.4e-135;
Matches 410; Conservative 3; Mismatches 6; Indels 9; Gaps 1;
QY 116 EPQLSCFRKSPLSNVVCEWGRSTPSLTTKAVILVRKFQNSPAEDFOEPCQYSESQKFS 175
DB 1 EPQLSCFRKSPLSNVVCEWGRSTPSLTTKAVILVRKFQNSPAEDFOEPCQYSESQKFS 60
QY 176 COLAVPEGDSSFYIVSMCVASSVSGSKFTQTFQCGILQDPDPANITVTVAARNPRLSV 235
DB 61 COLAVPEGDSSFYIVSMCVASSVSGSKFTQTFQCGILQDPDPANITVTVAARNPRLSV 120
QY 236 VTMODPHSNNSFYRLRFELRYRARSKTFTTMMVKDLOHHCVIDHWSGLRHVVOLRAO 295
DB 121 VTMODPHSNNSFYRLRFELRYRARSKTFTTMMVKDLOHHCVIDHWSGLRHVVOLRAO 180
QY 296 BEFGQSEWSEWSPAMGTPWTESRSPPAENEVSTPMQALITTKDDNILFRDSANATSLP 355
DB 181 BEFGQSEWSEWSPAMGTPWTESRSPPAENEVSTPMQALITTKDDNILSELV----- 234
QY 356 VEFMPVPPGEDSKDVAAPHROPULTSSERIDKQIRIYILDGISAARKETCNKSNMCESSKEA 415
DB 235 ---APVPPGEDSKDVAAPHROPULTSSERIDKQIRIYILDGISAARKETCNKSNMCESSKEA 291
QY 416 LAENNUNLPRKAEKDCGFCFSGFNEETCLVKIITGILEFEVYLEYIQRNRPESSEBOARAVO 475
DB 292 LAENNUNLPRKAEKDCGFCFSGFNEETCLVKIITGILEFEVYLEYIQRNRPESSEBOARAVO 351
QY 476 MSTKVLIOFLQKKAKNLDAITTPDPTNASTLTTLQAOQOMLQDMTTHLILRSFKFLOSSLRAL 535
DB 352 MSTKVLIOFLQKKAKNLDAITTPDPTNASTLTTLQAOQOMLQDMTTHLILRSFKFLOSSLRAL 411
QY 536 SUPALROM 543
DB 412 SUPALROM 419

RESULT 7
AAW70797
ID AAW70797 standard; protein; 592 AA.
XX
AC AAW70797;
XX
DT 03-FEB-1999 (first entry)
XX
DE Human interleukin-6R-alpha-Fc.
XX
KW gp130; cytokine antagonist; interleukin; gamma-interferon;
XX
KW granulocyte macrophage colony-stimulating factor; J peptide;
XX
KW transforming growth factor-beta.
XX
OS Synthetic.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Protein 1..358
FT /note="human IL-R-alpha"
FT Peptide 1..19
FT /note="signal peptide"

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FT	Misc-difference	2	/label= 12V
FT			/note= "changed to accomodate a Kozak sequence"
FT	Misc-difference	359.360	
FT			/note= "Ala-Gly bridge"
FT	Protein	361..592	
FT		/note= "Fc domain of human IgG1"	
FT	Dipeptide-bond	371..374	
XX			
PX	US5844099-A.		
PX			
PD	01-DEC-1998.		
XX			
PF	27-NOV-1995;	95US-00563105.	
PR	20-OCT-1993;	93US-00140222.	
XX			
PA	(REG-) REGENERON PHARM INC.		
XX			
PI	Yancopoulos GD, Stahl N, Economides A;		
XX			
DR	WPI; 1999-044669/04.		
XX			
PT	Cytokine antagonists - comprising extracellular domains of specificity-		
XX	determining and signal-transducing components of cytokine receptor.		
PS	Example 3; Fig 5; 46pp; English.		
XX			
CC	The present sequence represents the amino acid sequence of human		
CC	interleukin (IL)-6R-alpha-Fc. The protein is used in the course of the		
CC	invention. The specification describes cytokine antagonists comprising of		
CC	only the extracellular domain of the specificity-determining component of		
CC	the cytokine receptor and the extracellular domain of a signal-		
CC	transducing component of the cytokine receptor. The cytokine is an		
CC	interleukin (IL-1, IL-2, IL-3, IL-4, IL-5 or IL-15), granulocyte		
CC	macrophage colony-stimulating factor (GM-CSF), gamma-interferon or		
CC	transforming growth factor-beta (TGF-beta). The antagonist is capable of		
CC	binding the cytokine to form a nonfunctional complex. The compounds have		
CC	therapeutic activity as cytokine antagonists and can also be used in		
CC	assays for identifying novel agonists and antagonists of cytokines		
XX			
SQ	Sequence 592 AA:		
	Query Match	67.1%; Score 1921; DB 2; Length 592;	
	Best Local Similarity	77.1%; Pred. No. 4.2e-120;	
	Matches 377; Conservative 22; Mismatches 44; Indels 46; Gaps 5		
Oy	1	MLAVGCALIALAIPGALAPRALPRCPAQEVARGVLTSLPDSVTLTTCPGVEPEDNATVTHM	60
Db	1	MVANGCALIALAIALAPGALAPRALPRCPAQEVARGVLTSLPDSVTLTTCPGVEPEDNATVTHM	60
Oy	61	VLRPAAGSHPSRAAGGRLLRLRSVDLHDSGNVSCVRAGRPGVTHLVLDVPEEPOLLS	120
Db	61	VLRPAAGSHPSRAAGGRLLRLRSVDLHDSGNVSCVRAGRPGVTHLVLDVPEEPOLLS	120
Oy	121	CFRKSPLSNVVCWGPSTPSLTITKAVLVLRKFQNSPAEDFOEPCOYSQSQCFCOLAY	180
Db	121	CFRKSPLSNVVCWGPSTPSLTITKAVLVLRKFQNSPAEDFOEPCOYSQSQCFCOLAY	180
Oy	181	PEGSSFTIVMCVAASSVGSKFSKTQFOGGILOPPNPANITVTAARPMISVTWOD	240
Db	181	PEGSSFTIVMCVAASSVGSKFSKTQFOGGILOPPNPANITVTAARPMISVTWOD	240
Oy	241	PHSNWSFYRRFLRYFAERSKTFETTMVNDLOHCVIHDAMSGLRHVQLRAQEERFG	300
Db	241	PHSNWSFYRRFLRYFAERSKTFETTMVNDLOHCVIHDAMSGLRHVQLRAQEERFG	300
Oy	301	GEMSWASPEANGTPTESRSRPAAENSVETPMOALTNNKDNIIFRDSANNTSLPVFMFP	360
Db	301	GEMSWASPEANGTPTESRSRPAAENSVETPMOALTNNKDNIIFRDSANNTSLPVFMFP	360
Oy	361	VPPGDSDKVAPAPHOPQTSSSERIDKOIRYLIDGISALRKETCNKSINCE--SSKEALAE	418
Db	361	VPPGDSDKVAPAPHOPQTSSSERIDKOIRYLIDGISALRKETCNKSINCE--SSKEALAE	418

[illegible]

binding the cytokine to form a non-functional complex. The receptor components are shared by cytokines such as the CNTF (cellary neurotrophic factor) family of cytokines. The invention provides the basis for the development of IL-6 antagonists, as they show that if, in the presence of a ligand, a non-functional intermediate complex, consisting of the ligand, its alpha receptor and its beta-1 receptor component, can be formed, it will effectively block the action of the ligand. Effective antagonists of IL-6 or CNTF consist of heterodimers of the extracellular domains of the alpha specificity determining components of their receptors and the extracellular domain of gp130. The resultant heterodimers, function as high-affinity traps, rendering the cytokine inaccessible to form a signal transducing complex with the native membrane-bound forms of their receptor. The nucleic acids and polypeptides are useful for treating cytokine-related diseases or disorders such as osteoporosis and primary and secondary effects of cancer including multiple myeloma or cachexia

Sequence 592 AA;

Query Match 67.1%; Score 1921; DB 3; Length 592;
Best Local Similarity 77.1%; Pred. No. 4, 2e-120;
Matches 377; Conservative 22; Mismatches 44; Indels 46; Gaps 5;

1 MLAVGALIAALLAAGALAPRCPCAOEVARGVLTSLPGDSVTLTCPGVEPEDNATVHM 60
1 MVAVGALIAALLAAGALAPRCPCAOEVARGVLTSLPGDSVTLTCPGVEPEDNATVHM 60
61 VLRKPAAGSHPRMAGMGRLLRLRSVQLHDSGNYSCYRAGRAGTVHLLVDVPEEPQLS 120
61 VLRKPAAGSHPRMAGMGRLLRLRSVQLHDSGNYSCYRAGRAGTVHLLVDVPEEPQLS 120
121 CFRKSPLSNVVCEWGRSTPSTLTAKVLLVRKFNPSPADFPQPCQYSGESQKFSQCLAV 180
121 CFRKSPLSNVVCEWGRSTPSTLTAKVLLVRKFNPSPADFPQPCQYSGESQKFSQCLAV 180
181 PGDSSFYIVSMCVASSVSGSKSTQTFQCGCIIOPDPANITVTAANPRLSTWQD 240
181 PGDSSFYIVSMCVASSVSGSKSTQTFQCGCIIOPDPANITVTAANPRLSTWQD 240
241 PHSWNSFYRLRFLRYRARSKTFTTMMVKDLQHNHCIVHDAMSGLRHVYQLRAQEEFQ 300
241 PHSWNSFYRLRFLRYRARSKTFTTMMVKDLQHNHCIVHDAMSGLRHVYQLRAQEEFQ 300
301 GEMSEWSPAMGTPWTESRSPPAENEVSTPMQALTTNKDDNILLFRDSANATSLPVEFMP 360
301 GEMSEWSPAMGTPWTESRSPPAENEVSTPMQALTTNKDDNILLFRDSANATSLPVEFMP 360
361 VPPGEDSKDVAAPHROPLTSSERIDKQIRYIILDGISALRKETCKNSMCE--SSKEALAE 418
361 VPPGEDSKDVAAPHROPLTSSERIDKQIRYIILDGISALRKETCKNSMCE--SSKEALAE 418
419 NNUNLPKMAEKQCGFCGNEETCLVKIIT--GLLEFVYLEYLQ--NRFSSEEQAR 472
419 NNUNLPKMAEKQCGFCGNEETCLVKIIT--GLLEFVYLEYLQ--NRFSSEEQAR 472
473 AVQWSTKVL 481
473 AVQWSTKVL 481
443 STYRRVSVL 451
443 STYRRVSVL 451

RESULT 9
ABW02165
ID ABW02165 standard; protein; 592 AA.

ABW02165;
12-FEB-2004 (first entry)
Human IL-6Ralpha-Fc protein.
Cytokine; cytokine-related disease; immunomodulator; osteoporosis;
cancer; cachexia; arthritis; cyostatic; osteopathic; therapy; human.

OS Homo sapiens.

Key location/Qualifiers
Peptide 1..19
Protein /label= Signal_peptide
Region /note= "Human mature IL-6Ralpha-Fc protein"
Domain /note= "Ala-Gly bridge"
Disulfide-bond /note= "Human IgG1 Fc domain"
Disulfide-bond /note= "Inter-chain disulfide bridge"

US2003143697-A1.

31-JUL-2003.

28-OCT-2002; 2002US-00282162.

22-SEP-1999; 99WO-US022045.

22-MAR-2001; 2001US-00787835.

(STAH/) STAHL N.

(YANC/) YANCOPOULOS G D.

Stahl N, Yancopoulos GD.

WPI; 2003-851784/79.

New nucleic acid molecules encoding fusion polypeptides capable of

binding a cytokine to form a non-functional complex, useful for

treating cytokine-related diseases or disorders, e.g. cancer, cachexia, arthritis,

or osteoporosis.

Example 3; Fig 5; 300pp; English.

The present invention provides a novel fusion polypeptide capable of

binding a cytokine to form a nonfunctional complex. The invention is

useful for identifying agonists or antagonists of cytokine receptors and

for treating cytokine-related diseases or disorders e.g. cancer,

cachexia, arthritis and osteoporosis. The present sequence is human IL-

6Ralpha-Fc protein

Sequence 592 AA;

Query Match 67.1%; Score 1921; DB 7; Length 592;

Best Local Similarity 77.1%; Pred. No. 4, 2e-120;
Matches 377; Conservative 22; Mismatches 44; Indels 46; Gaps 5;

1 MLAVGALIAALLAAGALAPRCPCAOEVARGVLTSLPGDSVTLTCPGVEPEDNATVHM 60
1 MVAVGALIAALLAAGALAPRCPCAOEVARGVLTSLPGDSVTLTCPGVEPEDNATVHM 60
61 VLRKPAAGSHPRMAGMGRLLRLRSVQLHDSGNYSCYRAGRAGTVHLLVDVPEEPQLS 120
61 VLRKPAAGSHPRMAGMGRLLRLRSVQLHDSGNYSCYRAGRAGTVHLLVDVPEEPQLS 120
121 CFRKSPLSNVVCEWGRSTPSTLTAKVLLVRKFNPSPADFPQPCQYSGESQKFSQCLAV 180
121 CFRKSPLSNVVCEWGRSTPSTLTAKVLLVRKFNPSPADFPQPCQYSGESQKFSQCLAV 180
181 PGDSSFYIVSMCVASSVSGSKSTQTFQCGCIIOPDPANITVTAANPRLSTWQD 240
181 PGDSSFYIVSMCVASSVSGSKSTQTFQCGCIIOPDPANITVTAANPRLSTWQD 240
241 PHSWNSFYRLRFLRYRARSKTFTTMMVKDLQHNHCIVHDAMSGLRHVYQLRAQEEFQ 300
241 PHSWNSFYRLRFLRYRARSKTFTTMMVKDLQHNHCIVHDAMSGLRHVYQLRAQEEFQ 300
301 GEMSEWSPAMGTPWTESRSPPAENEVSTPMQALTTNKDDNILLFRDSANATSLPVEFMP 360
301 GEMSEWSPAMGTPWTESRSPPAENEVSTPMQALTTNKDDNILLFRDSANATSLPVEFMP 360
361 VPPGEDSKDVAAPHROPLTSSERIDKQIRYIILDGISALRKETCKNSMCE--SSKEALAE 418
361 VPPGEDSKDVAAPHROPLTSSERIDKQIRYIILDGISALRKETCKNSMCE--SSKEALAE 418
419 NNUNLPKMAEKQCGFCGNEETCLVKIIT--GLLEFVYLEYLQ--NRFSSEEQAR 472
419 NNUNLPKMAEKQCGFCGNEETCLVKIIT--GLLEFVYLEYLQ--NRFSSEEQAR 472
473 AVQWSTKVL 481
473 AVQWSTKVL 481
443 STYRRVSVL 451
443 STYRRVSVL 451

QY 361 VPPGEDSKVAAPHROPLTSSEKIDKQIRYIIDGISAALKETCKNSMNC--SSKEALAE 418
 Db 358 -----DAGEP-----KSCDKTHICTPCCPAPELLGG 382
 QY 419 NNINLPKMAEKDCFCFSGFNEETCLVKIT---GLIEFVYLEYLQ---NRESESEQAR 472
 Db 383 PSVFLPFPKPKDITLMSRTPEVTCVVVDVSHEDPEVKFMWYDGVENNAKTKPREEQYN 442
 QY 473 AVQMSTKVL 481
 Db 443 STYRVVSVL 451

RESULT 10
 AAP90284
 ID AAP90284 standard; protein; 468 AA.
 AC AAP90284;
 XX
 AC 25-MAR-2003 (revised)
 DT 31-MAR-1992 (first entry)
 XX
 DE Sequence of a receptor protein for human B cell stimulating factor-2
 DE (BSF2 receptor).
 XX
 KM B cell; immune disorder; therapy; diagnosis; prophylaxis.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH Region 2..22
 FT /label= hydrophobic region
 FT Region 362..386
 FT /label= hydrophobic region
 FT
 FT EP325474-A.
 PN 26-JUL-1989.
 PD
 XX 20-JAN-1989; 89EP-00300536.
 XX
 XX 22-JAN-1988; 88UP-00012387.
 PR 25-JAN-1988; 88UP-00012599.
 PR 04-AUG-1988; 88UP-00194885.
 PR 14-JAN-1989; 89JP-00007461.
 XX
 XX (KISH/) KISHIMOTO T.
 PA
 XX Kishimoto T.
 PI
 XX WPI; 1989-214667/30.
 DR N-PSDB; AAN90340.
 XX
 XX Receptor protein for human B cell stimulating factor-2 - obtd. by
 PT recombinant DNA techniques and used as diagnostic prophylactic or
 PT therapeutic agent.
 PT
 XX Claim 2; Page 19-21; 63pp; English.
 PS
 XX The cDNA in AAN90340 was derived from monocytic cell line U937. Isolated
 CC BSF2 receptor and DNA encoding it are claimed, as are (b) expression
 CC vectors; (c) host organisms; (d) antibodies; and (e) hybridomas. (Updated
 CC on 25-MAR-2003 to correct PR field.)
 CC
 XX Sequence 468 AA;
 SQ

Query March 67.0%; Score 1918; DB 1; Length 468;
 Best local similarity 96.5%; Pred. No. 5e-120;
 Matches 360; Conservative 1; Mismatches 4; Indels 8; Gaps 1;
 QY 1 MLAVGCALLAALLAAGALAPRCPPAEGVARGVLTSLPGDSVTLTCGVEPEDNATVHM 60
 |||

Db 1 MLAVGCALLAALLAAGALAPRCPPAEGVARGVLTSLPGDSVTLTCGVEPEDNATVHM 60
 QY 61 VLKRPAGSHSPSWAGKGRLLIRSVQLHDSGNYSCYRAGRAGVYHLLVDVPEEPOLS 120
 Db 61 VLKRPAGSHSPSWAGKGRLLIRSVQLHDSGNYSCYRAGRAGVYHLLVDVPEEPOLS 120
 QY 121 CFRKSPLSNVNCGMRPSTPSLTTKAVLLVRKFONSPAEDFOEPCQYSGESQKFSQOLAV 180
 Db 121 CFRKSPLSNVNCGMRPSTPSLTTKAVLLVRKFONSPAEDFOEPCQYSGESQKFSQOLAV 180
 QY 181 PEGDSFPIVSMCVASSVSGSKFSTQTFQCCGILQDPDPANTVTVAANPMHLSYTMQD 240
 Db 181 PEGDSFPIVSMCVASSVSGSKFSTQTFQCCGILQDPDPANTVTVAANPMHLSYTMQD 240
 QY 241 PHSWNSFPYRLRFLRYARSKTFTTMVVKDLOHHCVIHDAWSGLRHVVQLRAQEEFQ 300
 Db 241 PHSWNSFPYRLRFLRYARSKTFTTMVVKDLOHHCVIHDAWSGLRHVVQLRAQEEFQ 300
 QY 301 GEMSEWSPFAMGTPWTSRSPPAENEVSTPMQALTTKDDNLLFRDSANATSLPVBFMP 360
 Db 301 GEMSEWSPFAMGTPWTSRSPPAENEVSTPMQALTTKDDNLLFRDSANATSLPV---- 356
 QY 361 VPPGEDSKVAAP 373
 Db 357 ----QDSGVPLP 365

RESULT 11
 AAR37215
 ID AAR37215 standard; protein; 468 AA.
 XX
 XX AAR37215;
 AC
 XX 13-SEP-1993 (first entry)
 DT
 XX IL-6 receptor.
 DE
 XX Interleukin-6; IL-6; receptor; immunoglobulin-like; domain; truncated;
 KM transmembrane; multiple myeloma; binding; ability; signal transfer;
 KM disease; intracellular.
 KM
 XX Synthetic.
 OS
 XX JP05091892-A.
 PN
 XX 16-APR-1993.
 PD
 XX 02-OCT-1991; 91JP-00255521.
 XX
 XX 02-OCT-1991; 91JP-00255521.
 XX
 XX 02-OCT-1991; 91JP-00255521.
 PR
 XX (KISH/) KISHIMOTO C.
 PA (CHUS) CHUGAI PHARM CO LTD.
 PA (TOYJ) TOSOH CORP.
 XX
 XX WPI; 1993-161739/20.
 DR N-PSDB; AAQ41746.
 DR
 PT New interleukin-6 receptor deriv. - for treating diseases caused by IL-6,
 PT e.g. multiple myeloma.
 PT
 XX Disclosure; Page 10-12; 23pp; Japanese.
 PS
 XX This sequence represents an interleukin-6 (IL-6) receptor. Variants of
 CC the receptor lacking either the immunoglobulin-like domain or the
 CC transmembrane and intracellular domain have IL-6 binding ability and
 CC signal transfer ability. Either the full length or truncated IL-6
 CC receptors may be used for diseases caused by IL-6 such as multiple
 CC myeloma
 CC
 XX Sequence 468 AA;
 SQ

Query Match 67.0%; Score 1918; DB 2; Length 468;
 |||

Best Local Similarity 96.5%; Pred. No. 5e-120;
Matches 360; Conservative 1; Mismatches 4; Indels 8; Gaps 1;

```

QY 1 MLAVGALLAALLAAGALAPRCAPQAVAGVLTSLPGDSVTLTCTPGVEPDNATVHW 60
DB 1 MLAVGALLAALLAAGALAPRCAPQAVAGVLTSLPGDSVTLTCTPGVEPDNATVHW 60
QY 61 VLKRPAGSHPSRMAGMRLLRLRSVOLHDSGNYSCYRAGRPAQTVHLLVDVPEEPOLS 120
DB 61 VLKRPAGSHPSRMAGMRLLRLRSVOLHDSGNYSCYRAGRPAQTVHLLVDVPEEPOLS 120
QY 121 CRRKSPLSNVVCEWGRSTPSLTITKAIVLVKRFQNSPADPQPCQYQSQKFSQCLAV 180
DB 121 CRRKSPLSNVVCEWGRSTPSLTITKAIVLVKRFQNSPADPQPCQYQSQKFSQCLAV 180
QY 181 PEDSSFFIYVSMCVASVSGSKFSTQTFQCGGILQDPDPANITVTAVANPRSLSTWOD 240
DB 181 PEDSSFFIYVSMCVASVSGSKFSTQTFQCGGILQDPDPANITVTAVANPRSLSTWOD 240
QY 241 PSHMNSFYRLRPELRYRARSKTFTTMVVKDLQHHCVIHDAMSGLRHVVLRAQBEFQ 300
DB 241 PSHMNSFYRLRPELRYRARSKTFTTMVVKDLQHHCVIHDAMSGLRHVVLRAQBEFQ 300
QY 301 GEMSEWSPAMGTPWTESRSPPAENEVSTPMQALTTNKDDNILLFRDSANATSLPVEFMP 360
DB 301 GEMSEWSPAMGTPWTESRSPPAENEVSTPMQALTTNKDDNILLFRDSANATSLPVEFMP 360
QY 361 VPPGEDSKDVAAP 373
DB 357 ----QDSSSVPLP 365

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RESULT 12

AA36655
ID AAB36655 standard; protein; 468 AA.

AC AAB36655;

DT 13-MAR-2001 (first entry)

DE Human IL-6 receptor subunit alpha protein SEQ ID NO:12.

XX DNAX cytokine receptor subunit; DCRS2; receptor protein;

KW modulating cell proliferation; diagnosis; detection; drug screening;

KM immunological disorder.

OS Homo sapiens.

PN WO200073451-A1.

PD 07-DEC-2000.

PF 30-MAY-2000; 2000WO-US014867.

PR 01-JUN-1999; 99US-00322913.

PA (SCHE) SCHERING CORP.

PI Dowling LM, Timans JC, Gorman DM, Kastelein RA, Bazan FJ;

DR WPI; 2001-061536/07.

XX Novel composition comprising DNAX cytokine receptor subunit polypeptide

XX useful for regulating immune system function and for treating

XX immunological disorders.

XX Disclosure; Page 13-15; 93pp; English.

XX The present invention describes a composition (I) comprising a

XX recombinant DNAX cytokine receptor subunit-2 (DCRS2) polypeptide. The

XX DCRS2 polypeptide is useful for binding ligands and for preparing

XX antibodies. The DCRS2 polypeptide is also useful for modulating cell

XX proliferation, for diagnostic and therapeutic applications, for detecting

CC presence of their ligands and in drug screening assays. It is also useful

CC for treating conditions such as immunological disorder. The present

CC sequence represents a cytokine receptor subunit protein which is given in

CC an alignment of various cytokine receptor subunits in the exemplification

CC of the present invention

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Sequence 468 AA;

Query Match 67.0%; Score 1918; DB 4; Length 468;

Best Local Similarity 96.5%; Pred. No. 5e-120;

Matches 360; Conservative 1; Mismatches 4; Indels 8; Gaps 1;

```

QY 1 MLAVGALLAALLAAGALAPRCAPQAVAGVLTSLPGDSVTLTCTPGVEPDNATVHW 60
DB 1 MLAVGALLAALLAAGALAPRCAPQAVAGVLTSLPGDSVTLTCTPGVEPDNATVHW 60
QY 61 VLKRPAGSHPSRMAGMRLLRLRSVOLHDSGNYSCYRAGRPAQTVHLLVDVPEEPOLS 120
DB 61 VLKRPAGSHPSRMAGMRLLRLRSVOLHDSGNYSCYRAGRPAQTVHLLVDVPEEPOLS 120
QY 121 CRRKSPLSNVVCEWGRSTPSLTITKAIVLVKRFQNSPADPQPCQYQSQKFSQCLAV 180
DB 121 CRRKSPLSNVVCEWGRSTPSLTITKAIVLVKRFQNSPADPQPCQYQSQKFSQCLAV 180
QY 181 PEDSSFFIYVSMCVASVSGSKFSTQTFQCGGILQDPDPANITVTAVANPRSLSTWOD 240
DB 181 PEDSSFFIYVSMCVASVSGSKFSTQTFQCGGILQDPDPANITVTAVANPRSLSTWOD 240
QY 241 PSHMNSFYRLRPELRYRARSKTFTTMVVKDLQHHCVIHDAMSGLRHVVLRAQBEFQ 300
DB 241 PSHMNSFYRLRPELRYRARSKTFTTMVVKDLQHHCVIHDAMSGLRHVVLRAQBEFQ 300
QY 301 GEMSEWSPAMGTPWTESRSPPAENEVSTPMQALTTNKDDNILLFRDSANATSLPVEFMP 360
DB 301 GEMSEWSPAMGTPWTESRSPPAENEVSTPMQALTTNKDDNILLFRDSANATSLPVEFMP 360
QY 361 VPPGEDSKDVAAP 373
DB 357 ----QDSSSVPLP 365

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RESULT 13

AAE28593
ID AAE28593 standard; protein; 468 AA.

AC AAE28593;

DT 27-DEC-2002 (first entry)

DE Interleukin6 receptor (IL6R).

XX Hypoxia-regulated condition; tumorigenesis; angiogenesis; retinopathy;

KW inflammation; apoptosis; erythropoiesis; peripheral arterial disease;

KM cancer; ischemia; coronary arterial disease; inflammatory condition;

KW rheumatoid arthritis; reperfusion injury; neonatal stress; infection;

KM stroke; pre-eclampsia; atherosclerosis; cystic fibrosis; wound healing;

KW gene therapy; vaccine; interleukin receptor; IL6R.

XX Unidentified.

XX

XX

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XX

XX

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XX

DR WPI; 2002-698656/75.
DR N-PSDB; AAD45938.
XX
PT New hypoxia-regulated genes and polypeptides, useful for treating or
PT preventing hypoxia-regulated condition, e.g. tumorigenesis, angiogenesis,
PT inflammation, erythropoiesis, or the biological response to hypoxia
PT conditions.
XX
PS Claim 1; Page 106; 122pp; English.
XX
XX The invention relates to novel hypoxia-regulated polypeptides and
CC polynucleotides. Sequences of the invention are useful in therapy or
CC diagnosis of disease, particularly a hypoxia-regulated condition such as
CC tumorigenesis, angiogenesis, apoptosis, inflammation, erythropoiesis, or
CC the biological response to hypoxia conditions (including processes such
CC as glycolysis, gluconeogenesis, catecholamine synthesis, glucose
CC transport, iron transport or nitric oxide synthesis). They are also
CC useful in therapy or diagnosis of diseases or conditions affected by
CC hypoxia, e.g. cancer, ischaemic conditions (such as stroke, coronary or
CC peripheral arterial disease), reperfusion injury, neonatal stress,
CC retinopathy, preclampsia, atherosclerosis, inflammatory conditions
CC (including rheumatoid arthritis), diseases involving infections of the
CC always (such as cystic fibrosis) and wound healing. The invention is
CC useful in gene therapy and as vaccines. The present sequence is
CC interleukin-6 receptor (IL6R). This sequence is used in the
CC exemplification of the invention
XX
SQ Sequence 468 AA;
Query Match 67.0%; Score 1918; DB 5; Length 468;
Best Local Similarity 96.5%; Pred. No. 5e-120;
Matches 360; Conservative 1; Mismatches 4; Indels 8; Gaps 1;
QY 1 MLAVGICALALALAPGALAPRCPCPAQEVARGVLTSLPGDSVTLTCPGVEPDNATVHW 60
DB 1 MLAVGICALALALAPGALAPRCPCPAQEVARGVLTSLPGDSVTLTCPGVEPDNATVHW 60
QY VLKRPAGSHPSRWAGRGRLILRSVOLHDSGNYSYCRAGRPAGTVHLVDVPEEPQLS 120
DB VLKRPAGSHPSRWAGRGRLILRSVOLHDSGNYSYCRAGRPAGTVHLVDVPEEPQLS 120
QY 61 VLKRPAGSHPSRWAGRGRLILRSVOLHDSGNYSYCRAGRPAGTVHLVDVPEEPQLS 120
DB 61 VLKRPAGSHPSRWAGRGRLILRSVOLHDSGNYSYCRAGRPAGTVHLVDVPEEPQLS 120
QY 121 CFRKSPLSNVVCEWGPSTSLTTKAVILVRKFQNSPAEDFOEPCQYSQESQKFSQCLAV 180
DB 121 CFRKSPLSNVVCEWGPSTSLTTKAVILVRKFQNSPAEDFOEPCQYSQESQKFSQCLAV 180
QY 121 CFRKSPLSNVVCEWGPSTSLTTKAVILVRKFQNSPAEDFOEPCQYSQESQKFSQCLAV 180
DB 121 CFRKSPLSNVVCEWGPSTSLTTKAVILVRKFQNSPAEDFOEPCQYSQESQKFSQCLAV 180
QY 181 PEGDSFYIVSMCVASSVSGSKFTQTFQCGILQPPPANITVTAARNRMLSVTWOD 240
DB 181 PEGDSFYIVSMCVASSVSGSKFTQTFQCGILQPPPANITVTAARNRMLSVTWOD 240
QY 241 PHSNNSFYRLRFELRYARSKTFTTMWVKDLOHCVIHDAMSGLRHVQLRAQEEFGQ 300
DB 241 PHSNNSFYRLRFELRYARSKTFTTMWVKDLOHCVIHDAMSGLRHVQLRAQEEFGQ 300
QY 301 GEMSEMSPEAMGTPTWESRSPPAENEVSTPMQALITNKDDNILLFRDSANATSLPYEEMP 360
DB 301 GEMSEMSPEAMGTPTWESRSPPAENEVSTPMQALITNKDDNILLFRDSANATSLPYEEMP 360
QY 361 VPGEEDSKDVAAP 373
DB 357 ----QDSSSVLP 365

RESULT 14
ABB78191
ID ABB78191 standard; protein; 468 AA.
XX ABB78191;
XX
XX 05-NOV-2002 (first entry)
XX
XX Amino acid sequence of human interleukin-6 (IL-6) receptor alpha.
XX
XX Human; interleukin-6; IL-6 receptor alpha; IL-6 receptor alpha; IL-6; hepatocyte;

KM hepatitis B virus; HBV; glycoprotein 130; gp130; glycoprotein 80; gp80;
KM hepatitis B infection; ss.
XX
XX Homo sapiens.
XX US6410009-B1.
XX
XX 25-JUN-2002.
XX
XX 12-NOV-1999; 99US-00439856.
XX
XX 11-FEB-1997; 97US-00795473.
XX
XX (HADA-) HADASIT MEDICAL RES SERVICES & DEV.
XX Galun E, Nahor O, Blum HE;
XX
XX WPI; 2002-582017/62.
XX
XX Inhibiting or treating infection of hepatocytes by hepatitis B virus
PT using soluble agent which inhibits interaction between hIL-6 and
PT hepatocytes, particularly hyper-IL-6.
XX
XX Disclosure; Fig 9a-b; 38pp; English.
XX
XX The present sequence represents a human interleukin-6 (IL-6) receptor
CC alpha (IL-6R alpha). Fragments of IL-6 are used in the method of the
CC invention. The specification describes a method for inhibiting or
CC treating infection of hepatocytes by hepatitis B virus (HBV). The method
CC comprises administering to a human patient a soluble active agent which
CC inhibits interaction between human IL-6 and hepatocytes, and so inhibits
CC activation of glycoprotein 130 (gp130) and the internalisation of HBV
CC into the hepatocytes. The soluble agent is selected from glycoprotein 80
CC (gp80), or its portion spanning amino acids 113-323 and having receptor
CC sites that interact with IL6 and competitively inhibit interaction
CC between IL-6 and hepatocytes; glycoprotein 130 (gp130), or its portion
CC spanning amino acids 1-94 and 141-230 and having receptor sites that
CC interact with IL-6 and competitively inhibit interaction between IL-6 and
CC hepatocytes; IL-6 peptides LYS41-ALA56, GLY77-GLU95 or GLN153-HIS165;
CC and/or a combined beta1 and beta2 IL-6 mutant. The method is used to
CC prevent or treat hepatitis B infection
XX
XX Sequence 468 AA;
SQ
Query Match 67.0%; Score 1918; DB 5; Length 468;
Best Local Similarity 96.5%; Pred. No. 5e-120;
Matches 360; Conservative 1; Mismatches 4; Indels 8; Gaps 1;
QY 1 MLAVGICALALALAPGALAPRCPCPAQEVARGVLTSLPGDSVTLTCPGVEPDNATVHW 60
DB 1 MLAVGICALALALAPGALAPRCPCPAQEVARGVLTSLPGDSVTLTCPGVEPDNATVHW 60
QY 61 VLKRPAGSHPSRWAGRGRLILRSVOLHDSGNYSYCRAGRPAGTVHLVDVPEEPQLS 120
DB 61 VLKRPAGSHPSRWAGRGRLILRSVOLHDSGNYSYCRAGRPAGTVHLVDVPEEPQLS 120
QY 121 CFRKSPLSNVVCEWGPSTSLTTKAVILVRKFQNSPAEDFOEPCQYSQESQKFSQCLAV 180
DB 121 CFRKSPLSNVVCEWGPSTSLTTKAVILVRKFQNSPAEDFOEPCQYSQESQKFSQCLAV 180
QY 121 CFRKSPLSNVVCEWGPSTSLTTKAVILVRKFQNSPAEDFOEPCQYSQESQKFSQCLAV 180
DB 121 CFRKSPLSNVVCEWGPSTSLTTKAVILVRKFQNSPAEDFOEPCQYSQESQKFSQCLAV 180
QY 181 PEGDSFYIVSMCVASSVSGSKFTQTFQCGILQPPPANITVTAARNRMLSVTWOD 240
DB 181 PEGDSFYIVSMCVASSVSGSKFTQTFQCGILQPPPANITVTAARNRMLSVTWOD 240
QY 241 PHSNNSFYRLRFELRYARSKTFTTMWVKDLOHCVIHDAMSGLRHVQLRAQEEFGQ 300
DB 241 PHSNNSFYRLRFELRYARSKTFTTMWVKDLOHCVIHDAMSGLRHVQLRAQEEFGQ 300
QY 301 GEMSEMSPEAMGTPTWESRSPPAENEVSTPMQALITNKDDNILLFRDSANATSLPYEEMP 360
DB 301 GEMSEMSPEAMGTPTWESRSPPAENEVSTPMQALITNKDDNILLFRDSANATSLPYEEMP 360
QY 361 VPGEEDSKDVAAP 373

Db 357 ----QDSSSVPLP 365

RESULT 15
ABP72697
ID ABP72697 standard; protein; 468 AA

AC ABP72697;

DT 11-JUN-2003 (first entry)
XX

Human interleukin-6 receptor.

KW Human; interleukin-6; receptor; antibacterial; virucide; anti-HIV;
KW antirheumatic; antiarthritic; antiinflammatory; immunosuppressive;
KW gene therapy.

OS Homo sapiens.

Key	location/Qualifiers
FH	359, .386
FT	
FT	/label= Transmembrane

PN MO2003014359-A2.

PD 20-FEB-2003

02-AUG-2002; 2002WO-GB003581.

PR 03-AUG-2001; 2001GB-00019015

PA	(UYCA-)	UNIV COLLEGE CARDIFF.
PA	(UYWA-)	UNIV WALES COLLEGE OF MEDICINE

PI Jones SA, Topley N;

DR WPI; 2003-256588/25.

PT New fusion protein having a functional IL-6 and DS-βIL-6R molecule, PT useful for the manufacture of a medicament for the prophylaxis or PT treatment of an infectious disease, and an inflammatory or immunological PT disorder.

PS Disclosure; Fig 2; 46pp; English.

The present sequence is the protein sequence of the human interleukin-6 receptor (IL-6R). A soluble receptor is obtained either through proteolytic cleavage or differential mRNA splicing of IL-6R (see ABP72698). The present invention relates to a fusion protein (see ABP72702) comprising a functional IL-6 molecule and a functional DS-IL-6R molecule. Administration of the fusion protein results in the increased expression of one or more of MIP-1alpha, MIP-1beta, RANTES or IP-10. Also claimed are a nucleic acid molecule encoding the fusion protein, an expression vector, a host cell, and a method of producing the fusion protein in the host cell. The fusion protein, nucleic acid or vector can be used in the manufacture of a medicament for the prophylaxis or treatment of an infectious disease (especially AIDS caused by a M-tropic strain of HIV, or bacterial peritonitis), an inflammatory disorder or an immunological disorder (especially rheumatoid arthritis), when it is desirable to increase or resolve an immune response (claimed).

Query Match	67.0%	Score 1918;	DB 6;	Length 468;
Best Local Similarity	96.5%	Pred. No. 5e-120;		
Matches 360;	Conservative 1;	Mismatches 4;	Indels 8;	Gaps 1

Qy	Db	Qy	Db
1	1	1	1
MLAVGALLLAALAA	MLAVGALLLAALAA	MLAVGALLLAALAA	MLAVGALLLAALAA
PCGAEVPRCP	PCGAEVPRCP	PCGAEVPRCP	PCGAEVPRCP
AEVAGVLTLS	AEVAGVLTLS	AEVAGVLTLS	AEVAGVLTLS
LPDSDYTLTC	LPDSDYTLTC	LPDSDYTLTC	LPDSDYTLTC
PCPGVEPDDNATVYM	PCPGVEPDDNATVYM	PCPGVEPDDNATVYM	PCPGVEPDDNATVYM
6 C	6 C	6 C	6 C
1	1	1	1
MLAVGALLLAALAA	MLAVGALLLAALAA	MLAVGALLLAALAA	MLAVGALLLAALAA
PCGAEVPRCP	PCGAEVPRCP	PCGAEVPRCP	PCGAEVPRCP
AEVAGVLTLS	AEVAGVLTLS	AEVAGVLTLS	AEVAGVLTLS
LPDSDYTLTC	LPDSDYTLTC	LPDSDYTLTC	LPDSDYTLTC
PCPGVEPDDNATVYM	PCPGVEPDDNATVYM	PCPGVEPDDNATVYM	PCPGVEPDDNATVYM
6 C	6 C	6 C	6 C
61	61	61	61
VLRPAAGSHPSRWAGNGRRLLRSVQ	VLRPAAGSHPSRWAGNGRRLLRSVQ	VLRPAAGSHPSRWAGNGRRLLRSVQ	VLRPAAGSHPSRWAGNGRRLLRSVQ
LDHDSGNVSCYRAGRPAQTVHL	LDHDSGNVSCYRAGRPAQTVHL	LDHDSGNVSCYRAGRPAQTVHL	LDHDSGNVSCYRAGRPAQTVHL
LDVDPPEEPQLS	LDVDPPEEPQLS	LDVDPPEEPQLS	LDVDPPEEPQLS
1	1	1	1

Db	61	YAKPKAGHGHPSSMAGMGRRLLRLRSVOLHDSGNYSCTYAGRPACTVHLVLVDVPEEPBOLS	120
Qy	121	CFPKSPLSNVVCEMGGPRSTPSLTTTAVVLLVRFQMSPAEDFQOECCOYQSOESOKFS	160
Db	121	CFKSPSLSNVCEMGGPRSTPSLTTTAVVLLVRFQMSPAEDFQOECCOYQSOESOKFS	160
Qy	181	PEGDSSFYIVSVCVASSVSGSKFSTQTOGCGIILQDPDPANITTTAVARNRMLSTVMOD	240
Db	181	PEGDSSFYIVSVCVASSVSGSKFSTQTOGCGIILQDPDPANITTTAVARNRMLSTVMOD	240
Qy	241	PHSMNSSPFLRLPELRYRAERSKFTTMMVVDLQHHCVIHNAMSGLRHVVLRAQEEFGQ	300
Db	241	PHSMNSSPFLRLPELRYRAERSKFTTMMVVDLQHHCVIHNAMSGLRHVVLRAQEEFGQ	300
Qy	301	GEMSEWSPEAKGTPMTESRSPAEANEVSTPMQALTTNKDDNILLFRDSANATSLPVEFMP	360
Db	301	GEMSEWSPEAKGTPMTESRSPAEANEVSTPMQALTTNKDDNILLFRDSANATSLPVEFMP	360
Qy	361	VPPGSDSKVLAAP	373
Db	357	----QDSSSVPLP	365

RESULT 16
ADCO7187
ID ADCO7187 standard; protein; 468 AA

AC ADC07187
VV

DT 18-DEC-2003 (first entry)
 VV

Human IL-6 receptor subunit alpha

KM DNA cytokine receptor subunit 2; DCRS2; cell physiology;
KM cell development; cell culture; interferon detection;
KM immune system disorder; interleukin 6; IL-6; receptor subunit alpha
KM human.

OS Homo sapiens
xy

PN US2003082734-A1

PD 01-MAY-2003

PF 18-SEP-2002; 2002US-00247463

PR 01-JUN-1999; 99US-0137159P.

2000

PA (DOWL/) DOWLING L M.
PA (TIMA/) TIMANS J C.
PA (GORM/) GORMAN D M.
PA (KAST/) KASTELEIN R A.
PA (BAZA/) BAZAN J F.

PI Dowling LM, Timans JC, Gorman DM, Kastelein RA, Bazan JF,
XX
DR WPI; 2003-730048/69.

PT Composition potentially useful for treating immunological disorders,
PT comprising a DNAX cytokine receptor subunit 2 (DCRS2) polypeptide, a
PT natural DCRS2 polypeptide, or a fusion polypeptide comprising a DCRS2
PT sequence.

PS Disclosure; SEQ ID NO 12; 41pp; English.

CC The invention describes a composition of matter (i) comprising a
CC substantially pure or recombinant DNA cytokine receptor subunit 2
CC (DCKS2) polypeptide, a natural DCKS2 polypeptide, or a fusion protein
CC comprising a DCKS2 sequence. A composition of matter comprises: a
CC substantially pure or recombinant DCKS2 polypeptide comprising at least
CC three distinct nonoverlapping segments of at least four amino acids

CC identical to segments of a fully defined 384 amino acid sequence (S1),
 CC given in the specification; a substantially pure or recombinant DCRS2
 CC polypeptide comprising at least two distinct nonoverlapping segments of
 CC at least five amino acids identical to segments of S1; a natural sequence
 CC DCRS2 comprising S1; or a fusion polypeptide comprising a DCRS2 sequence.
 CC An agonist or antagonist of a mammalian DCRS2 is useful for modulating
 CC physiology or development of a cell or cell culture. Antibodies to a
 CC DCRS2 can be used for quantitative detection of interferon. The DCRS2
 CC polypeptides and nucleic acids and their binding agents are potentially
 CC useful in treating and diagnosing disease, especially disease associated
 CC with the immune system. This is the amino acid sequence of human
 CC interleukin 6 (IL-6) receptor subunit alpha used in a comparison with
 CC DCRS2.

XX Sequence 468 AA;

Query Match 67.0%; Score 1918; DB 7; Length 468;

Best Local Similarity 96.5%; Pred. No. 5e-120;

Matches 360; Conservative 1; Mismatches 4; Indels 8; Gaps 1;

QY 1 MLAVGALLAALAAPAALAPRRCPAQRVAVRGVLTSLPDSVTLLTCGVEPEDNATVHM 60
 DB 1 MLAVGALLAALAAPAALAPRRCPAQRVAVRGVLTSLPDSVTLLTCGVEPEDNATVHM 60
 QY 61 VLKRPAGSHPSRWAGMGRLLRSVQLHDSGNVSCYRAGRPAQTVHLVDVPEEPQLS 120
 DB 61 VLKRPAGSHPSRWAGMGRLLRSVQLHDSGNVSCYRAGRPAQTVHLVDVPEEPQLS 120
 QY 121 CFRKSPLSNVVCEWGPSTPSLTITKAVLLVRKFQNSPAEDFOEQYQSQKFSQCLAV 180
 DB 121 CFRKSPLSNVVCEWGPSTPSLTITKAVLLVRKFQNSPAEDFOEQYQSQKFSQCLAV 180
 QY 181 PEGDSSFYIVSMCVASSVGSKFSTQFOCGGIIQPPPNITVTAAARPRMLSTVMOD 240
 DB 181 PEGDSSFYIVSMCVASSVGSKFSTQFOCGGIIQPPPNITVTAAARPRMLSTVMOD 240
 QY 241 PHSNNSFYRLRFELRYARERKFTFTTMVYKDLQHCYIHDAWSGLRHVVQLRAQEEFGQ 300
 DB 241 PHSNNSFYRLRFELRYARERKFTFTTMVYKDLQHCYIHDAWSGLRHVVQLRAQEEFGQ 300
 QY 301 GEMSEWPEAMGTPWTSRSPPAENEVSTPMQALTNNKDDNIIFRDSANATSLPVEFMP 360
 DB 301 GEMSEWPEAMGTPWTSRSPPAENEVSTPMQALTNNKDDNIIFRDSANATSLPVEFMP 360
 QY 361 VPBGEDSKDVAAP 373
 DB 357 ---QDSSSVPLP 365

RESULT 17

AA92195
 ID AA92195 standard; protein; 690 AA.

XX AAY92195;

DT 01-AUG-2000 (first entry)

XX Human IL-6R-alpha-C-gamma-1 fusion protein.

XX IL-6R-alpha-C-gamma-1; cytokine; antagonist; CNTF; receptor;
 KW fusion protein; cytostatic; immunomodulator; osteopathic.

XX Synthetic.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Protein 1..358

FT Peptide 359..360

FT Protein /note= "Ala-Gly bridge"

FT Protein 361..690

XX /label= C-gamma-4

PN MO200018932-A2.

XX 06-APR-2000.

XX 22-SEP-1999; 99MO-US022045.

XX 25-SEP-1998; 98US-0101858P.

XX 19-MAY-1999; 99US-00313942.

XX (REGG-) REGENERON PHARM INC.

XX Stahl N, Yancopoulos GD;

XX WPI; 2000-293165/25.

PT Isolated nucleic acid molecule for treating cytokine-related diseases or
 PT disorders encodes a fusion polypeptide capable of binding a cytokine to
 PT form a nonfunctional complex.

XX Example 4; Page; 152pp; English.

XX The invention concerns production of antagonists to any cytokine that
 CC utilizes an alpha specificity determining component, which when combined
 CC with the cytokine, binds to a first beta signal transducing component to
 CC form a non-functional intermediate which then binds to a second beta
 CC signal transducing component causing beta-receptor dimerization, the
 CC soluble alpha specificity determining component of the receptor (SR-
 CC alpha) and the extracellular domain of the first beta signal transducing
 CC component of the cytokine receptor (beta-1) are combined to form
 CC heterodimers (SR-alpha:beta-1) that act as antagonist to the cytokine by
 CC binding the cytokine to form a non-functional complex. The receptor
 CC components are shared by cytokines such as the CNTF (ciliary neurotrophic
 CC factor) family of cytokines. The invention provides the basis for the
 CC development of IL-6 antagonists, as they show that if, in the presence of
 CC a ligand, a non-functional intermediate complex, consisting of the
 CC ligand, its alpha receptor and its beta-1 receptor component, can be
 CC formed, it will effectively block the action of the ligand. Effective
 CC antagonists of IL-6 or CNTF consist of heterodimers of the extracellular
 CC domains of the alpha specificity determining components of their
 CC receptors and the extracellular domain of gp130. The resultant
 CC heterodimers function as high-affinity traps, rendering the cytokine
 CC inaccessible to form a signal transducing complex with the native
 CC membrane-bound forms of their receptor. The nucleic acids and
 CC polypeptides are useful for treating cytokine-related diseases or
 CC disorders such as osteoporosis and primary and secondary effects of
 CC cancer including multiple myeloma or cachexia

XX Sequence 690 AA;

Query Match 67.0%; Score 1917; DB 3; Length 690;

Best Local Similarity 68.9%; Pred. No. 9.4e-120;

Matches 385; Conservative 29; Mismatches 57; Indels 88; Gaps 8;

QY 1 MLAVGALLAALAAPAALAPRRCPAQRVAVRGVLTSLPDSVTLLTCGVEPEDNATVHM 60
 DB 1 MLAVGALLAALAAPAALAPRRCPAQRVAVRGVLTSLPDSVTLLTCGVEPEDNATVHM 60
 QY 61 VLKRPAGSHPSRWAGMGRLLRSVQLHDSGNVSCYRAGRPAQTVHLVDVPEEPQLS 120
 DB 61 VLKRPAGSHPSRWAGMGRLLRSVQLHDSGNVSCYRAGRPAQTVHLVDVPEEPQLS 120
 QY 121 CFRKSPLSNVVCEWGPSTPSLTITKAVLLVRKFQNSPAEDFOEQYQSQKFSQCLAV 180
 DB 121 CFRKSPLSNVVCEWGPSTPSLTITKAVLLVRKFQNSPAEDFOEQYQSQKFSQCLAV 180
 QY 181 PEGDSSFYIVSMCVASSVGSKFSTQFOCGGIIQPPPNITVTAAARPRMLSTVMOD 240
 DB 181 PEGDSSFYIVSMCVASSVGSKFSTQFOCGGIIQPPPNITVTAAARPRMLSTVMOD 240
 QY 241 PHSNNSFYRLRFELRYARERKFTFTTMVYKDLQHCYIHDAWSGLRHVVQLRAQEEFGQ 300
 DB 241 PHSNNSFYRLRFELRYARERKFTFTTMVYKDLQHCYIHDAWSGLRHVVQLRAQEEFGQ 300

XX PN WO9618416-A1.
 XX PD 20-JUN-1996.
 XX PF 15-DEC-1995; 95WO-JF002587.
 XX PR 16-DEC-1994; 94JP-00313167.
 XX PR 18-AUG-1995; 95JP-00210739.
 XX PA (CHUS) CHUGAI SEIYAKU KK.
 XX PI Kuromaru K, Koishibara Y;
 XX PI WPI; 1996-300392/30.
 XX DR N-PSDB; AAT31441.
 XX PT Anti-sense oligo:nucleotide inhibitor against human IL-6R expression -
 XX PT for treatment of e.g. tumours, cancers, rheumatoid arthritis, psoriasis,
 XX PT endo:toxic shock, etc.
 XX PS Claim 2; Page 17-21; 32pp; Japanese.
 XX CC Antisense oligonucleotides may be used to inhibit the expression of the
 XX CC interleukin-6 receptor. Inhibition of expression of the IL-6 receptor is
 XX CC useful in the treatment of kidney tumours, myeloma, Kaposi's sarcoma,
 XX CC rheumatoid arthritis, psoriasis and endotoxic shock. The antisense
 XX CC oligonucleotides are administered at a dosage of 0.1-100mg/kg, pref. 0.1-
 XX CC 50 mg/kg
 XX SQ Sequence 468 AA;
 XX
 Query Match 66.9%; Score 1915; DB 2; Length 468;
 Best Local Similarity 96.2%; Pred. No. 7.9e-120;
 Matches 359; Conservative 2; Mismatches 4; Indels 8; Gaps 1;

QY 1 MLAVGALLAALAAAPGALAPRCPAQEVARGVLTSLPGDSVTLTLCGVEPEDNATVHM 60
 DB 1 MLAVGALLAALAAAPGALAPRCPAQEVARGVLTSLPGDSVTLTLCGVEPEDNATVHM 60
 QY 61 VLKRPAGSHPSRWAGMGRLLRLRSVOLHDSGNVSCYRAGRPAQVHLLVDVPEEPQLS 120
 DB 61 VLKRPAGSHPSRWAGMGRLLRLRSVOLHDSGNVSCYRAGRPAQVHLLVDVPEEPQLS 120
 QY 121 CFRKSPLSNVCEWGPSTPSLTITKAVILVRFKONS PAEDFOBPQCOYSQESQKSCQLAV 180
 DB 121 CFRKSPLSNVCEWGPSTPSLTITKAVILVRFKONS PAEDFOBPQCOYSQESQKSCQLAV 180
 QY 181 PEGDSSFYIVSMCVASSVSGSKFSKTQTFQCGILQDPDPANITVTVAARNPRLSVTWOD 240
 DB 181 PEGDSSFYIVSMCVASSVSGSKFSKTQTFQCGILQDPDPANITVTVAARNPRLSVTWOD 240
 QY 241 PHSWNSFFYRLRFELRYRAERSKTFTTWAVKDLQHHCVIHDAMSGLRHVQVLAQAEFFQ 300
 DB 241 PHSWNSFFYRLRFELRYRAERSKTFTTWAVKDLQHHCVIHDAMSGLRHVQVLAQAEFFQ 300
 QY 301 GEKSEWSPKAMGTWTESRSPPAENEVSTPMQALTTNKDDNILFRDSANATSLPVEFWP 360
 DB 301 GEKSEWSPKAMGTWTESRSPPAENEVSTPMQALTTNKDDNILFRDSANATSLPVEFWP 360
 QY 361 VPPGEDSKDVAAP 373
 DB 357 ----QDSSSVPLP 365

RESULT 20
 ABP72699
 ID ABP72699 standard; protein; 357 AA.
 XX AC ABP72699;
 XX DT 11-JUN-2003 (first entry)
 XX

DE Soluble interleukin-6 receptor isoform PC-sIL-6R.
 XX Human; interleukin-6; receptor; PC-sIL-6R; antibacterial; virucide;
 XX anti-HIV; antirheumatic; antiarthritic; antiinflammatory;
 XX immunosuppressive; gene therapy.
 XX OS Homo sapiens.
 XX PN WO2003014359-A2.
 XX PD 20-FEB-2003.
 XX PF 02-AUG-2002; 2002WO-GB003581.
 XX PR 03-AUG-2001; 2001GB-00019015.
 XX PA (UYWA-) UNIV COLLEGE CARDIFF.
 XX PI (UYWA-) UNIV WALES COLLEGE OF MEDICINE.
 XX PI Jones SA, Topley N;
 XX PI WPI; 2003-256588/25.
 XX DR
 XX PT New fusion protein having a functional IL-6 and DS-sIL-6R molecule.
 XX PT useful for the manufacture of a medicament for the prophylaxis or
 XX PT treatment of an infectious disease, and an inflammatory or immunological
 XX PT disorder.
 XX PS Disclosure; Fig 2; 46pp; English.
 XX
 The present sequence is the protein sequence of a soluble form of the
 CC human interleukin-6 receptor (IL-6R), denoted PC-sIL-6R, produced by
 CC proteolytic cleavage. A fusion protein of human IL-6 and PC-sIL-6R
 CC increases expression of MCP-1, but unlike a novel fusion protein of the
 CC invention (see ABP72702) comprising IL-6 and DS-sIL-6R, does not increase
 CC expression of MIP-1alpha, MIP-1beta, RANTES or IP-10. The invention
 CC relates to this novel fusion protein and its use in the prophylaxis or
 CC treatment of an infectious disease (especially AIDS caused by a M-trophic
 CC strain of HIV, or bacterial peritonitis), an inflammatory disorder or an
 CC immunological disorder (especially rheumatoid arthritis), when it is
 CC desirable to increase or resolve an immune response
 XX SQ Sequence 357 AA;
 XX
 Query Match 66.9%; Score 1913; DB 6; Length 357;
 Best Local Similarity 99.7%; Pred. No. 7.7e-120;
 Matches 356; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLAVGALLAALAAAPGALAPRCPAQEVARGVLTSLPGDSVTLTLCGVEPEDNATVHM 60
 DB 1 MLAVGALLAALAAAPGALAPRCPAQEVARGVLTSLPGDSVTLTLCGVEPEDNATVHM 60
 QY 61 VLKRPAGSHPSRWAGMGRLLRLRSVOLHDSGNVSCYRAGRPAQVHLLVDVPEEPQLS 120
 DB 61 VLKRPAGSHPSRWAGMGRLLRLRSVOLHDSGNVSCYRAGRPAQVHLLVDVPEEPQLS 120
 QY 121 CFRKSPLSNVCEWGPSTPSLTITKAVILVRFKONS PAEDFOBPQCOYSQESQKSCQLAV 180
 DB 121 CFRKSPLSNVCEWGPSTPSLTITKAVILVRFKONS PAEDFOBPQCOYSQESQKSCQLAV 180
 QY 181 PEGDSSFYIVSMCVASSVSGSKFSKTQTFQCGILQDPDPANITVTVAARNPRLSVTWOD 240
 DB 181 PEGDSSFYIVSMCVASSVSGSKFSKTQTFQCGILQDPDPANITVTVAARNPRLSVTWOD 240
 QY 241 PHSWNSFFYRLRFELRYRAERSKTFTTWAVKDLQHHCVIHDAMSGLRHVQVLAQAEFFQ 300
 DB 241 PHSWNSFFYRLRFELRYRAERSKTFTTWAVKDLQHHCVIHDAMSGLRHVQVLAQAEFFQ 300
 QY 301 GEKSEWSPKAMGTWTESRSPPAENEVSTPMQALTTNKDDNILFRDSANATSLPVEFWP 357
 DB 301 GEKSEWSPKAMGTWTESRSPPAENEVSTPMQALTTNKDDNILFRDSANATSLPVEFWP 357

RESULT 21
AAV92197
ID AAV92197 standard; protein; 477 AA.
XX
AC AAV92197;
XX
DT 01-AUG-2000 (first entry)
XX
DE Human IL-6R-alpha-j-kappa fusion protein.
XX
KM IL-6R-alpha-j-kappa; cytokine; antagonist; CNTF; receptor;
XX fusion protein; cytosolic; immunomodulator; osteopathic.
XX
OS Synthetic.
XX Homo sapiens.
XX WO200018932-A2.
XX
XX 06-APR-2000.
XX
XX 22-SEP-1999; 99WO-US022045.
XX
XX 25-SEP-1998; 98US-0101858P.
XX 19-MAY-1999; 99US-00313942.
XX
XX (REG-) REGENERON PHARM INC.
XX
XX Stahl N, Yancopoulos GD;
XX
XX WPI; 2000-293165/25.
XX
XX Isolated nucleic acid molecule for treating cytokine-related diseases or
XX disorders encodes a fusion polypeptide capable of binding a cytokine to
XX form a nonfunctional complex.
XX
XX Example 4; Page; 152pp; English.
XX
XX The invention concerns production of antagonists to any cytokine that
XX utilizes an alpha specificity determining component, which when combined
XX with the cytokine, binds to a first beta signal transducing component to
XX form a non-functional intermediate which then binds to a second beta
XX signal transducing component causing beta-receptor dimerization, the
XX soluble alpha specificity determining component of the receptor (SR-
XX alpha) and the extracellular domain of the first beta signal transducing
XX component of the cytokine receptor (beta-1) are combined to form
XX heterodimers (SR-alpha:beta-1) that act as antagonist to the cytokine by
XX binding the cytokine to form a non-functional complex. The receptor
XX components are shared by cytokines such as the CNTF (ciliary neurotrophic
XX factor) family of cytokines. The invention provides the basis for the
XX development of IL-6 antagonists, as they show that if, in the presence of
XX a ligand, a non-functional intermediate complex, consisting of the
XX ligand, its alpha receptor and its beta-1 receptor component, can be
XX formed, it will effectively block the action of the ligand. Effective
XX antagonists of IL-6 or CNTF consist of heterodimers of the extracellular
XX domains of the alpha specificity determining components of their
XX receptors and the extracellular domain of gp130. The resultant
XX heterodimers, function as high-affinity traps, rendering the cytokine
XX inaccessible to form a signal transducing complex with the native
XX membrane-bound forms of their receptor. The nucleic acids and
XX polypeptides are useful for treating cytokine-related diseases or
XX disorders such as osteoporosis and primary and secondary effects of
XX cancer including multiple myeloma or cachexia
XX
XX Sequence 477 AA;

Query Match 66.8%; Score 1912; DB 3; Length 477;
Best Local Similarity 82.8%; Pred. No. 1.3e-119;
Matches 375; Conservative 13; Mismatches 25; Indels 40; Gaps 7;

QY 1 MAAVGCALLAALAAAGALAPRCRAQEVARGVLTSLPDSVTTLTCPCVPEPDNATVMW 60
DB 1 MAAVGCALLAALAAAGALAPRCRAQEVARGVLTSLPDSVTTLTCPCVPEPDNATVMW 60

QY 61 VLKRPAGSHPSRMWAGMRRLILRSVOLHDSGNVSCYRAGRPAQVHLVDPPEEPQLS 120
DB 61 VLKRPAGSHPSRMWAGMRRLILRSVOLHDSGNVSCYRAGRPAQVHLVDPPEEPQLS 120
QY 121 CFRKSPLSNVVCEWGRSTPSLTTKAVLLVRKFNQSPADPQPCQYSGESQKFSQCLAV 180
DB 121 CFRKSPLSNVVCEWGRSTPSLTTKAVLLVRKFNQSPADPQPCQYSGESQKFSQCLAV 180
QY 181 PGDSSFFYIVSMCVASVSGSKFSKTQTFQCGGILQDPDPANITTVAVANPRLSTYMOD 240
DB 181 PGDSSFFYIVSMCVASVSGSKFSKTQTFQCGGILQDPDPANITTVAVANPRLSTYMOD 240
QY 241 PHSWSSFFYRLRFLRYAERSKFTTMMVXDLQHHCVIHDAMSGLRHVQLRAGEFQ 300
DB 241 PHSWSSFFYRLRFLRYAERSKFTTMMVXDLQHHCVIHDAMSGLRHVQLRAGEFQ 300
QY 301 GEMSEWSPAMGTPTWESRSPPAENEVSFTPMQALTTNKDDNILLPDSANATSLPVQDAG 360
DB 301 GEMSEWSPAMGTPTWESRSPPAENEVSFTPMQALTTNKDDNILLPDSANATSLPVQDAG 360
QY 358 -FMPVPQGE---DSKDVAAAPHROPVLTSSERIDKOIRYILDGIALRKETCNKSNCESS 412
DB 361 TF---GGTVEIKTVAAAPSVFIFFPS---DEQK-----SGTASVVCILANF----- 402
QY 413 KEALAENNILPRMA---EKDGCFOGSPNEBT 441
DB 403 -----YPREAKVQKVNALQSGNSQGS 425

RESULT 22
AAW70804
ID AAW70804 standard; protein; 360 AA.
XX

AC AAW70804;

DT 03-FEB-1999 (first entry)

DE Amino acid sequence of the interleukin (IL)-6R-alpha domain.

KM gp130; cytokine antagonist; interleukin; gamma-interferon;

KW granulocyte macrophage colony-stimulating factor; J peptide;

XX transforming growth factor-beta.

OS Synthetic.

FX Key Location/Qualifiers

FT Protein 1..358 /note="soluble interleukin (IL)-6R-alpha domain"

PN US844099-A.

PD 01-DEC-1998.

PF 27-NOV-1995; 95US-00563105.

PR 20-OCT-1993; 93US-00140222.

PA (REG-) REGENERON PHARM INC.

PI Yancopoulos GD, Stahl N, Economides A;

DR WPI; 1999-044669/04.

PT Cytokine antagonists - comprising extracellular domains of specificity-

XX determining and signal-transducing components of cytokine receptor.

XX Example 4; Fig 15; 46pp; English.

XX The present sequence represents the amino acid sequence of interleukin

XX (IL)-6R-alpha domain. The protein is used in the course of the invention.

XX The specification describes cytokine antagonists comprising only the

XX extracellular domain of the specificity-determining component of the

XX cytokine receptor and the extracellular domain of a signal-transducing

CC component of the cytokine receptor. The cytokine is an interleukin (IL-1,
 CC IL-2, IL-3, IL-4, IL-5 or IL-15), granulocyte macrophage colony-
 CC stimulating factor (GM-CSF), gamma-interferon or transforming growth
 CC factor-beta (TGF-beta). The antagonist is capable of binding the cytokine
 CC to form a nonfunctional complex. The compound has therapeutic activity
 CC as cytokine antagonists and can also be used in assays for identifying
 CC novel agonists and antagonists of cytokines
 XX
 SQ Sequence 360 AA;
 Query Match 66.8%; Score 1910; DB 2; Length 360;
 Best Local Similarity 99.4%; Pred. No. 1,2e-119; Indels 0; Gaps 0;
 Matches 355; Conservative 2; Mismatches 0;
 QY 1 MNAVGCALLAALLAAGALAPRCPCPAQEVARGVLTSLPDSVTLTCPGVEPEDNATVHM 60
 Db 1 MNAVGCALLAALLAAGALAPRCPCPAQEVARGVLTSLPDSVTLTCPGVEPEDNATVHM 60
 QY 61 VLKPPAAGSHPSRWAGMGRLLRLRSVQLHDSGNVSCYRAGRPAQTVHLLVDVPEEPQLS 120
 Db 61 VLKPPAAGSHPSRWAGMGRLLRLRSVQLHDSGNVSCYRAGRPAQTVHLLVDVPEEPQLS 120
 QY 121 CFFKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYSGESQKFSQCLAV 180
 Db 121 CFFKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYSGESQKFSQCLAV 180
 QY 181 PEGDSSFYIVSMCVASVSGSKFSKTQTFQCGILQPPDPANITVTAVANPRMLSTVMQD 240
 Db 181 PEGDSSFYIVSMCVASVSGSKFSKTQTFQCGILQPPDPANITVTAVANPRMLSTVMQD 240
 QY 241 PHSWNSFYRLRPELRARERKFTTMMVKDLOHHCVIDHAWSGLRHVQLRAQEEFQG 300
 Db 241 PHSWNSFYRLRPELRARERKFTTMMVKDLOHHCVIDHAWSGLRHVQLRAQEEFQG 300
 QY 301 GEWSEWSPAMGTPWTESSRSPAEENEVSTPMQALTTNKDDNILLFDSANATSLPVE 357
 Db 301 GEWSEWSPAMGTPWTESSRSPAEENEVSTPMQALTTNKDDNILLFDSANATSLPVE 357
 RESULT 23
 AAY92199 standard; protein; 360 AA.
 XX
 AC AAY92199;
 DT 01-AUG-2000 (first entry)
 XX
 DE Soluble human IL-6-R-alpha.
 XX
 KW Soluble IL-6-R-alpha; cytokine; antagonist; CNTF; receptor;
 KW fusion protein; cytosolic; immunomodulator; osteopathic.
 XX
 OS Homo sapiens.
 XX
 PN WO200018932-A2.
 XX
 PD 06-APR-2000.
 XX
 PF 22-SEP-1999; 99WO-US022045.
 XX
 PR 25-SEP-1998; 98US-0101858P.
 PR 19-MAY-1999; 99US-00313942.
 XX
 PA (REGG-) REGENERON PHARM INC.
 XX
 PI Stahl N, Yancopoulos GD;
 XX
 DR WPI; 2000-293165/25.
 XX
 PT Isolated nucleic acid molecule for treating cytokine-related diseases or
 PT disorders encodes a fusion polypeptide capable of binding a cytokine to
 PT form a nonfunctional complex.
 XX

PS Example 4; Fig 15; 152pp; English.
 XX
 CC The invention concerns production of antagonists to any cytokine that
 CC utilizes an alpha specificity determining component, which when combined
 CC with the cytokine, binds to a first beta signal transducing component to
 CC form a non-functional intermediate which then binds to a second beta
 CC signal transducing component causing beta-receptor dimerization, the
 CC soluble alpha specificity determining component of the receptor (SR-
 CC alpha) and the extracellular domain of the first beta signal transducing
 CC component of the cytokine receptor (beta-1) are combined to form
 CC heterodimers (SR-alpha:beta-1) that act as antagonist to the cytokine by
 CC binding the cytokine to form a non-functional complex. The receptor
 CC components are shared by cytokines such as the CNTF (ciliary neurotrophic
 CC factor) family of cytokines. The invention provides the basis for the
 CC development of IL-6 antagonists, as they show that if, in the presence of
 CC a ligand, a non-functional intermediate complex, consisting of the
 CC ligand, its alpha receptor and its beta-1 receptor component, can be
 CC formed, it will effectively block the action of the ligand. Effective
 CC antagonists of IL-6 or CNTF consist of heterodimers of the extracellular
 CC domains of the alpha specificity determining components of their
 CC receptors and the extracellular domain of gp130. The resultant
 CC heterodimers, function as high-affinity traps, rendering the cytokine
 CC inaccessible to form a signal transducing complex with the native
 CC membrane-bound forms of their receptor. The nucleic acids and
 CC polypeptides are useful for treating cytokine-related diseases or
 CC disorders such as osteoporosis and primary and secondary effects of
 CC cancer including multiple myeloma or cachexia
 XX
 SQ Sequence 360 AA;
 Query Match 66.8%; Score 1910; DB 3; Length 360;
 Best Local Similarity 99.4%; Pred. No. 1,2e-119;
 Matches 355; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MNAVGCALLAALLAAGALAPRCPCPAQEVARGVLTSLPDSVTLTCPGVEPEDNATVHM 60
 Db 1 MNAVGCALLAALLAAGALAPRCPCPAQEVARGVLTSLPDSVTLTCPGVEPEDNATVHM 60
 QY 61 VLKPPAAGSHPSRWAGMGRLLRLRSVQLHDSGNVSCYRAGRPAQTVHLLVDVPEEPQLS 120
 Db 61 VLKPPAAGSHPSRWAGMGRLLRLRSVQLHDSGNVSCYRAGRPAQTVHLLVDVPEEPQLS 120
 QY 121 CFFKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYSGESQKFSQCLAV 180
 Db 121 CFFKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYSGESQKFSQCLAV 180
 QY 181 PEGDSSFYIVSMCVASVSGSKFSKTQTFQCGILQPPDPANITVTAVANPRMLSTVMQD 240
 Db 181 PEGDSSFYIVSMCVASVSGSKFSKTQTFQCGILQPPDPANITVTAVANPRMLSTVMQD 240
 QY 241 PHSWNSFYRLRPELRARERKFTTMMVKDLOHHCVIDHAWSGLRHVQLRAQEEFQG 300
 Db 241 PHSWNSFYRLRPELRARERKFTTMMVKDLOHHCVIDHAWSGLRHVQLRAQEEFQG 300
 QY 301 GEWSEWSPAMGTPWTESSRSPAEENEVSTPMQALTTNKDDNILLFDSANATSLPVE 357
 Db 301 GEWSEWSPAMGTPWTESSRSPAEENEVSTPMQALTTNKDDNILLFDSANATSLPVE 357
 RESULT 24
 ABW02172
 ID ABW02172 standard; protein; 360 AA.
 XX
 AC ABW02172;
 DT 12-FEB-2004 (first entry)
 XX
 DE Human IL-6Ralpha-domain protein.
 XX
 KW Cytokine; cytokine-related disease; immunomodulator; osteoporosis;
 KW cancer; cachexia; arthritis; cytosolic; osteopathic; therapy; human.
 XX
 OS Homo sapiens.

XX Key Location/Qualifiers
 FH Region 1..358 "Human IL-6/alpha-domain"
 FT /note="Human IL-6/alpha-domain"
 FT Region 99..100
 FT /note="Ala-Gly bridge"
 XX US2003143697-A1.
 XX 31-JUL-2003.
 XX 28-OCT-2002; 2002US-00282162.
 XX 22-SEP-1999; 99WO-US022045.
 PR 22-MAR-2001; 2001US-00787835.
 XX (STAHN/) STAHN N.
 PA (YANC/) YANCOPULOS G D.
 XX Stahl N, Yancopoulos GD;
 PI WPI, 2003-851784/79.
 XX New nucleic acid molecules encoding fusion polypeptides capable of
 PT binding a cytokine to form a non-functional complex, useful for treating
 PT cytokine-related diseases or disorders, e.g. cancer, cachexia, arthritis,
 PT or osteoporosis.
 XX Example 4; Fig 15; 300pp; English.
 XX The present invention provides a novel fusion polypeptide capable of
 CC binding a cytokine to form a nonfunctional complex. The invention is
 CC useful for identifying agonists or antagonists of cytokine receptors and
 CC for treating cytokine-related diseases or disorders e.g. cancer,
 CC cachexia, arthritis and osteoporosis. The present sequence is human IL-
 CC 6/alpha-domain protein
 XX
 XX Sequence 360 AA;
 SQ
 Query Match 66.8%; Score 1910; DB 7; Length 360;
 Best Local Similarity 99.4%; Pred. No. 1.2e-119;
 Matches 355; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLAVGALLAALLAAGALAPRCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHM 60
 DB 1 MVAVGALLAALLAAGALAPRCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHM 60
 QY 61 VLRKPAAGSHPSRWAGMGRRLILRSVQLHDSGNVSCYRAGRPAQTVHLLVDVPEEPOLS 120
 DB 61 VLRKPAAGSHPSRWAGMGRRLILRSVQLHDSGNVSCYRAGRPAQTVHLLVDVPEEPOLS 120
 QY 121 CFRKSPLSNVVCEWGRSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYSGESQKFSQCLAV 180
 DB 121 CFRKSPLSNVVCEWGRSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYSGESQKFSQCLAV 180
 QY 181 PEDSSFFIYVSMCVASSVSGSKSTQTFQCGGILQDPDPANITVTVAANPRMLSTWOD 240
 DB 181 PEDSSFFIYVSMCVASSVSGSKSTQTFQCGGILQDPDPANITVTVAANPRMLSTWOD 240
 QY 241 PHSWNSFFRLRFLRYRARSKTFTTMMVKDLOHHCVIDAMSGLRHVQLRAQEEFQG 300
 DB 241 PHSWNSFFRLRFLRYRARSKTFTTMMVKDLOHHCVIDAMSGLRHVQLRAQEEFQG 300
 QY 301 GEWSEWSPAMGTPWTESRSPPAENEVSTPMQALITNKDDNITLFRDSANATSLPVE 357
 DB 301 GEWSEWSPAMGTPWTESRSPPAENEVSTPMQALITNKDDNITLFRDSANATSLPVE 357
 RESULT 25
 AAP90525
 ID AAP90525 standard; protein; 468 AA.
 XX
 AC AAP90525;

XX 25-MAR-2003 (revised)
 DT 23-JAN-1990 (first entry)
 XX B cell stimulating factor-2 receptor.
 DE B cell stimulating factor-2 receptor.
 XX B cell stimulating factor-2 receptor; monocytic U937 cell line.
 OS Homo sapiens.
 XX AU8928720-A.
 XX 27-JUL-1989.
 XX 23-JAN-1989; 89AU-00028720.
 PR 14-JAN-1989; 89JP-00007461.
 XX (KISH/) KISHIMOTO T.
 PA WPI; 1989-264012/37.
 DR N-PSDB; AAP90525.
 XX Receptor protein for human B cell stimulatory factor-2 - used for
 PT developing prophylactic, therapeutic and diagnostic agents for associated
 PT disorders.
 XX Claim 2; Page 36; 76pp; English.
 XX The BSF2 receptor is derived from a monocytic U937 cell line. It can be
 CC used to develop prophylactic and therapeutic pharmaceuticals, as agents to
 CC relate diseases and disorders to abnormal BSF-2 prodn. It can also be
 CC used to study an immune mechanism with which BSF-2 or the receptor is
 CC concerned. (Updated on 25-MAR-2003 to correct PA field.)
 XX
 XX Sequence 468 AA;
 SQ
 Query Match 66.8%; Score 1910; DB 1; Length 468;
 Best Local Similarity 96.2%; Pred. No. 1.7e-119;
 Matches 359; Conservative 1; Mismatches 5; Indels 8; Gaps 1;
 QY 1 MLAVGALLAALLAAGALAPRCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHM 60
 DB 1 MVAVGALLAALLAAGALAPRCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHM 60
 QY 61 VLRKPAAGSHPSRWAGMGRRLILRSVQLHDSGNVSCYRAGRPAQTVHLLVDVPEEPOLS 120
 DB 61 VLRKPAAGSHPSRWAGMGRRLILRSVQLHDSGNVSCYRAGRPAQTVHLLVDVPEEPOLS 120
 QY 121 CFRKSPLSNVVCEWGRSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYSGESQKFSQCLAV 180
 DB 121 CFRKSPLSNVVCEWGRSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYSGESQKFSQCLAV 180
 QY 181 PEDSSFFIYVSMCVASSVSGSKSTQTFQCGGILQDPDPANITVTVAANPRMLSTWOD 240
 DB 181 PEDSSFFIYVSMCVASSVSGSKSTQTFQCGGILQDPDPANITVTVAANPRMLSTWOD 240
 QY 241 PHSWNSFFRLRFLRYRARSKTFTTMMVKDLOHHCVIDAMSGLRHVQLRAQEEFQG 300
 DB 241 PHSWNSFFRLRFLRYRARSKTFTTMMVKDLOHHCVIDAMSGLRHVQLRAQEEFQG 300
 QY 301 GEWSEWSPAMGTPWTESRSPPAENEVSTPMQALITNKDDNITLFRDSANATSLPVE 356
 DB 301 GEWSEWSPAMGTPWTESRSPPAENEVSTPMQALITNKDDNITLFRDSANATSLPVE 356
 RESULT 26
 ABP72698
 ID ABP72698 standard; protein; 364 AA.
 XX
 AC ABP72698;

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XX ABP72698;
AC
XX
DT 11-JUN-2003 (first entry)
DE Soluble interleukin-6 receptor isoform DS-sil-6R.
XX
XX Human; interleukin-6; receptor; DS-sil-6R; antibacterial; virucide;
XX anti-HIV; antipneumatic; antiarthritic; antiinflammatory;
XX immunosuppressive; gene therapy.
XX
OS Homo sapiens.
XX
XX WQ003014359-A2.
XX
XX 20-FEB-2003.
XX
XX 02-AUG-2002; 2002MO-GB003581.
XX
XX 03-AUG-2001; 2001GB-00019015.
XX
XX (UYCA-) UNIV COLLEGE CARDIFF.
XX (UYMA-) UNIV WALES COLLEGE OF MEDICINE.
XX
XX Jones SA, Topley N;
XX
XX WPI; 2003-256588/25.
XX
XX New fusion protein having a functional IL-6 and DS-sil-6R molecule,
XX useful for the manufacture of a medicament for the prophylaxis or
XX treatment of an infectious disease, and an inflammatory or immunological
XX disorder.
XX
XX Disclosure; Fig 4; 46pp; English.
XX
XX The present sequence is the protein sequence of a soluble form of the
XX human interleukin-6 receptor (IL-6R), denoted DS-sil-6R, produced by
XX differential mRNA splicing. The invention relates to a fusion protein
XX (see ABP72702) comprising a functional IL-6 molecule and a functional DS-
XX sil-6R molecule. Administration of the fusion protein results in the
XX increased expression of one or more of MIP-1alpha, MIP-1beta, RANTES or
XX IP-10. High levels of MIP-1alpha, MIP-1beta and RANTES complex with HIV
XX for binding to CCR5 and effectively suppress HIV entry. The fusion
XX protein can be used in the treatment of any disease in which the
XX infectious agent binds to CCR5, especially M-trophic strains of HIV. The
XX invention also provides a nucleic acid molecule encoding the fusion
XX protein, an expression vector, a host cell, and a method of producing the
XX fusion protein in the host cell. The fusion protein, nucleic acid or
XX vector can be used in the manufacture of a medicament for the prophylaxis
XX or treatment of an infectious disease (especially AIDS caused by a M-
XX tropic strain of HIV, or bacterial peritonitis), an inflammatory
XX disorder or an immunological disorder (especially rheumatoid arthritis),
XX when it is desirable to increase or resolve an immune response (claimed)
XX
XX
XX Sequence 364 AA;
XX
XX Query Match 66.7%; Score 1907; DB 6; Length 364;
XX Best Local Similarity 100.0%; Pred. No. 2e-119;
XX Matches 355; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 181 PEGDSSFYIVSMCVASSVSGSKFSKTQTFQCGGILQPPDPANITVTAARNRMLSVTWOD 240
QY 241 PHSNNSFFRLRRLRRLRYRERSTFTTMVKLOLCHHCYVHDMSGRLRHVVQVRAQREFG 300
DB 241 PHSNNSFFRLRRLRRLRYRERSTFTTMVKLOLCHHCYVHDMSGRLRHVVQVRAQREFG 300
QY 301 GEMSEMSPEAMGTPWTESRSPPAENEVSTPMQALTNKDDNITLFRDSANATSLP 355
DB 301 GEMSEMSPEAMGTPWTESRSPPAENEVSTPMQALTNKDDNITLFRDSANATSLP 355

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RESULT 27
AAW71371
ID AAW71371 standard; protein; 468 AA.
XX
XX
XX AAW71371;
XX
XX 02-FEB-1999 (first entry)
XX
XX Human interleukin-6 receptor alpha polypeptide.
XX
XX Interleukin-6 receptor; human; hepatitis B virus; HBV; infection;
XX therapy.
XX
XX Homo sapiens.
XX
XX WQ9835694-A2.
XX
XX 20-AUG-1998.
XX
XX 10-FEB-1998; 98MO-US008898.
XX
XX 11-FEB-1997; 97US-00795473.
XX
XX
XX (HADA-) HADASIT MEDICAL RES SERVICES & DEV.
XX (DAVI/) DAVIDSON C M.
XX
XX WPI; 1998-520755/44.
XX
XX Treatment of hepatitis B virus infection - using a soluble active agent
XX which prevents interaction of HBV with hepatocytes mediated by human
XX interleukin 6.
XX
XX Disclosure; Fig 9; 51pp; English.
XX
XX
XX This is a previously reported amino acid sequence for human interleukin-6
XX (hIL-6) receptor alpha. The invention relates to the finding that hIL-6
XX is essential for hepatitis B virus (HBV) infection. The invention
XX provides a pharmaceutical composition for the treatment of HBV infection,
XX comprising a soluble active agent that interacts with at least one of the
XX binding sites between hIL-6 and the psi region of HBV and between hIL-6
XX and hepatocytes and other HBV-permissive cells. The active agent
XX competitively binds to at least one of these sites and thereby prevents
XX hIL-6-mediated HBV infection of hepatocytes and other HBV-permissive
XX cells. The soluble active agent is selected from glycoprotein 80 (gp80)
XX having receptor sites which interact with hIL-6, soluble glycoprotein 130
XX (gp130) having receptor sites which interact with hIL-6, hIL-6 derived
XX peptide Lys41-Lys67, hIL-6 derived peptide Gly77-Glu95, hIL-6 derived
XX peptide Glu153-His165, a combined 1 and 2 hIL-6 mutant (mhIL-6 1+2) and
XX mhIL-6 1+2 substituted with Phe171 to Leu and Ser177 to Arg, and mixtures
XX of any of these
XX
XX
XX Sequence 468 AA;
XX
XX Query Match 66.4%; Score 1900; DB 2; Length 468;
XX Best Local Similarity 95.4%; Pred. No. 8e-119;
XX Matches 356; Conservative 5; Mismatches 4; Indels 8; Gaps 1;

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QY 1 MIAVGCALALALAAFGAALAPRRCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHW 60
DB 1 MIAVGCALALALAAFGAALAPRRCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHW 60

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CC study an immune mechanism with which BSF-2 or the receptor is concerned.
CC (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 344 AA:

Query Match 64.7%; Score 1852; DB 1; Length 344;
Best Local Similarity 100.0%; Pred. No. 9e-116;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVAAGCALIAALAAAGALAPRRCPAOGVARGVLTSLPGDSVTLTCGVEPEDNATVHM 60
DB 1 MVAAGCALIAALAAAGALAPRRCPAOGVARGVLTSLPGDSVTLTCGVEPEDNATVHM 60
QY 61 VLKPPAAGSHPRSMAGMRRLLRVSQVLDHSGNVCYRAGRPAQTVHLLVDVPEEPQLS 120
DB 61 VLKPPAAGSHPRSMAGMRRLLRVSQVLDHSGNVCYRAGRPAQTVHLLVDVPEEPQLS 120
QY 121 CFRKSPLSNVVCEWGRSTPSLTTKAVLLVRKQNSPAEDFOBPQYSQESQKFSQCLAV 180
DB 121 CFRKSPLSNVVCEWGRSTPSLTTKAVLLVRKQNSPAEDFOBPQYSQESQKFSQCLAV 180
QY 181 PEGDSSFYIVSMCVASVSGSKFKTQTFQCGGILQDPDPANITVTAVARNPRMLSVTMQD 240
DB 181 PEGDSSFYIVSMCVASVSGSKFKTQTFQCGGILQDPDPANITVTAVARNPRMLSVTMQD 240
QY 241 PHSWNSFFYRLRFLRYRAERSKTFTTMMVKDLOHCVIHDAMSGLRHVQLRAQEEFQ 300
DB 241 PHSWNSFFYRLRFLRYRAERSKTFTTMMVKDLOHCVIHDAMSGLRHVQLRAQEEFQ 300
QY 301 GEMSEMSPEAMGTPTWTSRSPPAENEVSTPMQALITTKDDNLL 344
DB 301 GEMSEMSPEAMGTPTWTSRSPPAENEVSTPMQALITTKDDNLL 344

RESULT 30

AA92205
ID AA92205 standard; protein; 1158 AA.

XX AC AA92205;

DT 01-AUG-2000 (first entry)

XX Fusion polypeptide 616, IL-6 trap.

DE IL-6 trap; cytokine; antagonist; CNTF; receptor; fusion protein;

KW cytosolic; immunomodulator; osteopathic.

XX Synthetic.

OS Homo sapiens.

XX WO200018932-A2.

PN 06-APR-2000.

XX 22-SEP-1999; 99WO-US022045.

XX 25-SEP-1998; 98US-0101858P.

XX 19-MAY-1999; 99US-00313942.

XX (REGG-) REGENERON PHARM INC.

XX Stahl N, Yancopoulos GD;

XX WPI, 2000-293165/25.

XX N-PSDB; AAA09047.

XX Isolated nucleic acid molecule for treating cytokine-related diseases or

XX PT disorders encodes a fusion polypeptide capable of binding a cytokine to

XX form a nonfunctional complex.

XX Example 6; Fig 25A-F; 152pp; English.

XX This sequence shows fusion polypeptide 616, which is capable of binding

CC cytokine IL-6 to form a non-functional complex. The invention concerns
CC production of antagonists to any cytokine that utilizes an alpha
CC specificity determining component, which when combined with the cytokine,
CC binds to a first beta signal transducing component to form a non-
CC functional intermediate which then binds to a second beta signal
CC transducing component causing beta-receptor dimerization, the soluble
CC alpha specificity determining component of the receptor (SR-alpha) and
CC the extracellular domain of the first beta signal transducing component
CC of the cytokine receptor (beta-1) are combined to form heterodimers (SR-
CC alpha:beta-1) that act as antagonist to the cytokine by binding the
CC cytokine to form a non-functional complex. The receptor components are
CC shared by cytokines such as the CNTF (ciliary neurotrophic factor) family
CC of cytokines. The invention provides the basis for the development of IL-
CC 6 antagonists, as they show that if, in the presence of a ligand, a non-
CC functional intermediate complex, consisting of the ligand, its alpha
CC receptor and its beta-1 receptor component, can be formed, it will
CC effectively block the action of the ligand. Effective antagonists of IL-6
CC or CNTF consist of heterodimers of the extracellular domains of the alpha
CC specificity determining components of their receptors and the
CC extracellular domain of gp130. The resultant heterodimers, function as
CC high-affinity traps, rendering the cytokine inaccessible to form a signal
CC transducing complex with the native membrane-bound forms of their
CC receptor. The nucleic acids and polypeptides are useful for treating
CC cytokine-related diseases or disorders such as osteoporosis and primary
CC and secondary effects of cancer including multiple myeloma or cachexia

XX Sequence 1158 AA:

Query Match 62.5%; Score 1788; DB 3; Length 1158;
Best Local Similarity 99.1%; Pred. No. 7.8e-111;
Matches 331; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MVAAGCALIAALAAAGALAPRRCPAOGVARGVLTSLPGDSVTLTCGVEPEDNATVHM 60
DB 1 MVAAGCALIAALAAAGALAPRRCPAOGVARGVLTSLPGDSVTLTCGVEPEDNATVHM 60
QY 61 VLKPPAAGSHPRSMAGMRRLLRVSQVLDHSGNVCYRAGRPAQTVHLLVDVPEEPQLS 120
DB 61 VLKPPAAGSHPRSMAGMRRLLRVSQVLDHSGNVCYRAGRPAQTVHLLVDVPEEPQLS 120
QY 121 CFRKSPLSNVVCEWGRSTPSLTTKAVLLVRKQNSPAEDFOBPQYSQESQKFSQCLAV 180
DB 121 CFRKSPLSNVVCEWGRSTPSLTTKAVLLVRKQNSPAEDFOBPQYSQESQKFSQCLAV 180
QY 181 PEGDSSFYIVSMCVASVSGSKFKTQTFQCGGILQDPDPANITVTAVARNPRMLSVTMQD 240
DB 181 PEGDSSFYIVSMCVASVSGSKFKTQTFQCGGILQDPDPANITVTAVARNPRMLSVTMQD 240
QY 241 PHSWNSFFYRLRFLRYRAERSKTFTTMMVKDLOHCVIHDAMSGLRHVQLRAQEEFQ 300
DB 241 PHSWNSFFYRLRFLRYRAERSKTFTTMMVKDLOHCVIHDAMSGLRHVQLRAQEEFQ 300
QY 301 GEMSEMSPEAMGTPTWTSRSPPAENEVSTPMQAL 334
DB 301 GEMSEMSPEAMGTPTWTSRSPPAENEVSTPMQAL 334

RESULT 31

ABW02178
ID ABW02178 standard; protein; 1158 AA.

XX AC ABW02178;

DT 12-FEB-2004 (first entry)

XX Human cytokine trap-616 protein.

XX Cytokine; cytokine-related disease; immunomodulator; osteoporosis;

XX cancer; cachexia; arthritis; cytosolic; osteopathic; therapy; human.

XX Homo sapiens.

XX US2003143697-A1.

XX 31-JUL-2003.
 PD Best Local Similarity 99.1%; Score 1788; DB 7; Length 1158;
 XX 28-OCT-2002; 2002US-00282162.
 XX
 XX 22-SEP-1999; 99WO-US022045.
 XX 22-MAR-2001; 2001US-00787835.
 XX
 XX (STAH/) STAHL N.
 XX (YANC/) YANCOPULOS G D.
 XX Stahl N, Yancopoulos GD;
 XX
 XX MPI: 2003-851784/79.
 XX N-PSDB; AAD63741.
 XX
 XX New nucleic acid molecules encoding fusion polypeptides capable of
 PT binding a cytokine to form a non-functional complex, useful for treating
 PT cytokine-related diseases or disorders, e.g. cancer, cachexia, arthritis,
 PT or osteoporosis.
 XX
 XX Disclosure; Fig 25; 300pp; English.
 XX
 XX The present invention provides a novel fusion polypeptide capable of
 CC binding a cytokine to form a nonfunctional complex. The invention is
 CC useful for identifying agonists or antagonists of cytokine receptors and
 CC for treating cytokine-related diseases or disorders e.g. cancer,
 CC cachexia, arthritis and osteoporosis. The present sequence is human
 CC cytokine trap protein
 CC
 XX Sequence 1158 AA;
 SQ

Query Match 62.5%; Score 1788; DB 7; Length 1158;
 Best Local Similarity 99.1%; Pred. No. 7.8e-110; Indels 0; Gaps 0;
 Matches 331; Conservative 2; Mismatches 1;
 QY 1 MLAVGCAALAAALAAAGALAPRCPAEOVARAVLTSLPGDSTVTLTCCPGVEPEDNATVHM 60
 DB 1 MVAAGCALAALAAALAAAGALAPRCPAEOVARAVLTSLPGDSTVTLTCCPGVEPEDNATVHM 60
 QY 61 VLRKPAAGSHPSRWAGMGRRLLRVSQVLDHSGNYSCTYRAGRPAAGTVHLLVDVPEEPOLLS 120
 DB 61 VLRKPAAGSHPSRWAGMGRRLLRVSQVLDHSGNYSCTYRAGRPAAGTVHLLVDVPEEPOLLS 120
 QY 121 CFRKSPLSNVVCEWGRSTPSLTTRKAVLVKRFQNSPADFOBPCCOYSOSQKFSQCLAV 180
 DB 121 CFRKSPLSNVVCEWGRSTPSLTTRKAVLVKRFQNSPADFOBPCCOYSOSQKFSQCLAV 180
 QY 181 PEGDSSFYIVSMCVASVSGSKFSKTOTFOGCGILQDPDPANITVTVAARPRMLSTWOD 240
 DB 181 PEGDSSFYIVSMCVASVSGSKFSKTOTFOGCGILQDPDPANITVTVAARPRMLSTWOD 240
 QY 241 PHSWNSFYRLRRELRYRAERSKFTTMMVKDLQHHCVIHDANSGLRHVVQJLAQEEFQ 300
 DB 241 PHSWNSFYRLRRELRYRAERSKFTTMMVKDLQHHCVIHDANSGLRHVVQJLAQEEFQ 300
 QY 301 GEMSEWSPRAGTPTWESRSRPPANEVSTPMOAL 334
 DB 301 GEMSEWSPRAGTPTWESRSRPPANEVSTPMOAL 334
 QY 301 GEMSEWSPRAGTPTWESRSRPPANEVSTPMELL 334
 DB 301 GEMSEWSPRAGTPTWESRSRPPANEVSTPMELL 334

RESULT 32
 ID AAY92204 standard; protein; 1168 AA.
 XX AAY92204;
 XX
 XX 01-ANG-2000 (first entry)
 XX
 XX Fusion polypeptide 412, IL-6 trap.
 XX
 XX IL-6 trap; cytokine; antagonist; CNTF; receptor; fusion protein;
 KW cytostatic; immunomodulator; osteopathic.

XX Synthetic.
 OS Homo sapiens.
 XX
 XX WO200018932-A2.
 XX
 XX 06-APR-2000.
 XX
 XX 22-SEP-1999; 99WO-US022045.
 XX
 XX 25-SEP-1998; 98US-0101858P.
 XX 19-MAY-1999; 99US-00313942.
 XX
 XX (REGG-) REGENERON PHARM INC.
 XX
 XX Stahl N, Yancopoulos GD;
 XX
 XX MPI: 2000-293165/25.
 XX N-PSDB; AAA09046.
 XX
 XX Isolated nucleic acid molecule for treating cytokine-related diseases or
 PT disorders encodes a fusion polypeptide capable of binding a cytokine to
 PT form a nonfunctional complex.
 XX
 XX Example 6; Fig 24A-F; 152pp; English.

This sequence shows fusion polypeptide 412, which is capable of binding
 CC cytokine IL-6 to form a non-functional complex. The invention concerns
 CC production of antagonists to any cytokine that utilizes an alpha
 CC specificity determining component, which when combined with the cytokine,
 CC binds to a first beta signal transducing component to form a non-
 CC functional intermediate which then binds to a second beta signal
 CC transducing component causing beta-receptor dimerization, the soluble
 CC alpha specificity determining component of the receptor (SR-alpha) and
 CC the extracellular domain of the first beta signal transducing component
 CC of the cytokine receptor (beta-1) are combined to form heterodimers (SR-
 CC alpha:beta-1) that act as antagonist to the cytokine by binding the
 CC cytokine to form a non-functional complex. The receptor components are
 CC shared by cytokines such as the CNTF (ciliary neurotrophic factor) family
 CC of cytokines. The invention provides the basis for the development of IL-
 CC 6 antagonists, as they show that if, in the presence of a ligand, a non-
 CC functional intermediate complex, consisting of the ligand, its alpha
 CC receptor and its beta-1 receptor component, can be formed, it will
 CC effectively block the action of the ligand. Effective antagonists of IL-6
 CC or CNTF consist of heterodimers of the extracellular domains of the alpha
 CC specificity determining components of their receptors and the
 CC extracellular domain of gp130. The resultant heterodimers, function as
 CC high-affinity traps, rendering the cytokine inaccessible to form a signal
 CC transducing complex with the native membrane-bound forms of their
 CC receptor. The nucleic acids and polypeptides are useful for treating
 CC cytokine-related diseases or disorders such as osteoporosis and primary
 CC and secondary effects of cancer including multiple myeloma or cachexia
 XX
 XX Sequence 1168 AA;
 SQ

Query Match 62.3%; Score 1783; DB 3; Length 1168;
 Best Local Similarity 99.7%; Pred. No. 1.7e-110; Indels 0; Gaps 0;
 Matches 330; Conservative 1; Mismatches 0;
 QY 1 MLAVGCAALAAALAAAGALAPRCPAEOVARAVLTSLPGDSTVTLTCCPGVEPEDNATVHM 60
 DB 1 MVAAGCALAALAAALAAAGALAPRCPAEOVARAVLTSLPGDSTVTLTCCPGVEPEDNATVHM 60
 QY 61 VLRKPAAGSHPSRWAGMGRRLLRVSQVLDHSGNYSCTYRAGRPAAGTVHLLVDVPEEPOLLS 120
 DB 61 VLRKPAAGSHPSRWAGMGRRLLRVSQVLDHSGNYSCTYRAGRPAAGTVHLLVDVPEEPOLLS 120
 QY 121 CFRKSPLSNVVCEWGRSTPSLTTRKAVLVKRFQNSPADFOBPCCOYSOSQKFSQCLAV 180
 DB 121 CFRKSPLSNVVCEWGRSTPSLTTRKAVLVKRFQNSPADFOBPCCOYSOSQKFSQCLAV 180
 QY 181 PEGDSSFYIVSMCVASVSGSKFSKTOTFOGCGILQDPDPANITVTVAARPRMLSTWOD 240
 DB 181 PEGDSSFYIVSMCVASVSGSKFSKTOTFOGCGILQDPDPANITVTVAARPRMLSTWOD 240

Db 181 PEGDSSFFYIVSMCVASSVGSKFSKTQTFQCGGILQDPDPANITVTVAARNPRMLSVTWOD 240
 QY 241 PHSWNSFFYRLRFELRYAERSKTFTTMMVKDLOHHCVHIDAMSGLRHVQQLRAQEEFGQ 300
 Db 241 PHSWNSFFYRLRFELRYAERSKTFTTMMVKDLOHHCVHIDAMSGLRHVQQLRAQEEFGQ 300
 QY 301 GEWSWSPAMGTPTWTSRSPPAENEVSTPM 331
 Db 301 GEWSWSPAMGTPTWTSRSPPAENEVSTPM 331

RESULT 33
 ABO2177
 ID ABO2177 standard; protein; 1168 AA.

AC ABO2177;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 DE Human cytokine trap-412 protein.
 XX
 DE Cytokine; cytokine-related disease; immunomodulator; osteoporosis;
 KW cancer; cachexia; arthritis; cytostatic; osteopathic; therapy; human.

XX Homo sapiens.
 OS
 XX US2003143697-A1.
 XX
 PD 31-JUL-2003.

XX 28-OCT-2002; 2002US-00282162.

XX 22-SEP-1999; 99WO-US022045.
 PR 22-MAR-2001; 2001US-00787835.

XX (STAHN/) STAHL N.
 PA (YANC/) YANCOPoulos G D.

PI Stahl N, Yancopoulos GD;

DR WPI; 2003-851784/79.
 N-PSDB; AAD63740.

PT New nucleic acid molecules encoding fusion polypeptides capable of
 binding a cytokine to form a non-functional complex, useful for treating
 cytokine-related diseases or disorders, e.g. cancer, cachexia, arthritis,
 or osteoporosis.

XX Example 8; Fig 24; 300bp; English.

XX The present invention provides a novel fusion polypeptide capable of
 binding a cytokine to form a nonfunctional complex. The invention is
 useful for identifying agonists or antagonists of cytokine receptors and
 for treating cytokine-related diseases or disorders e.g. cancer,
 cachexia, arthritis and osteoporosis. The present sequence is human
 cytokine trap protein

XX Sequence 1168 AA;

Query Match 62.3%; Score 1783; DB 7; Length 1168;
 Best Local Similarity 99.7%; Pred. No. 1,7e-110;
 Matches 330; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAVGGALLAALAAAGALAPRCPAOEVARGVLTSLGDSVTTLCPGVEPEDNATVAM 60
 Db 1 MVAVGGALLAALAAAGALAPRCPAOEVARGVLTSLGDSVTTLCPGVEPEDNATVAM 60
 QY 61 VLKRPAGSHPSRWAGGRLLRSVQLHDSGVSCYRAGRPAGTVHLLVDVPPESPOL 120
 Db 61 VLKRPAGSHPSRWAGGRLLRSVQLHDSGVSCYRAGRPAGTVHLLVDVPPESPOL 120
 QY 121 CFRKSPLSNVCEWGPSTPSLTTKAVLVKRFQNSPAEFPQCOYSOSOKFSCGLAV 180

Db 121 CFRKSPLSNVCEWGPSTPSLTTKAVLVKRFQNSPAEFPQCOYSOSOKFSCGLAV 180
 QY 181 PEGDSSFFYIVSMCVASSVGSKFSKTQTFQCGGILQDPDPANITVTVAARNPRMLSVTWOD 240
 Db 181 PEGDSSFFYIVSMCVASSVGSKFSKTQTFQCGGILQDPDPANITVTVAARNPRMLSVTWOD 240
 QY 241 PHSWNSFFYRLRFELRYAERSKTFTTMMVKDLOHHCVHIDAMSGLRHVQQLRAQEEFGQ 300
 Db 241 PHSWNSFFYRLRFELRYAERSKTFTTMMVKDLOHHCVHIDAMSGLRHVQQLRAQEEFGQ 300
 QY 301 GEWSWSPAMGTPTWTSRSPPAENEVSTPM 331
 Db 301 GEWSWSPAMGTPTWTSRSPPAENEVSTPM 331

RESULT 34
 AAO23014
 ID AAO23014 standard; protein; 325 AA.

AC AAO23014;
 XX
 DT 17-SEP-2003 (first entry)
 XX
 DE Human interleukin 6 receptor alpha chain wild-type peptide.

XX Cytostatic; antiinflammatory; antirheumatic; anti-arthritis; anti-HIV;
 KW nephrotropic; osteopathic; antipsoriatic; interleukin-6 receptor; IL-6R;
 KW alpha chain; cytokine; multiple myeloma; lymphoma; inflammation; sepsis;
 KW rheumatoid arthritis; prostate cancer; Castleman's disease; AIDS; human;
 KW mesangial proliferative glomerulonephritis; Kaposi's sarcoma; psoriasis;
 KW osteoporosis; protein co-ordinate data; wild-type.

XX Homo sapiens.

XX Location/Qualifiers

FT Key 1..93
 FT Domain /note= "D1 domain"

FT 1..5 /note= "Dimer interface, at which IL-6R monomers interact
 to form a homodimer"

FT 6..174 /label= Disulfide_bond
 FT 19..23

FT /note= "Dimer interface, at which IL-6R monomers interact
 to form a homodimer"

FT 65..69 /note= "Dimer interface, at which IL-6R monomers interact
 to form a homodimer"

FT 93..99 /note= "Dimer interface, at which IL-6R monomers interact
 to form a homodimer"

FT 94..194 /note= "D2 domain"

FT 94..95 /note= "Double proline motif"

FT 106..110 /note= "I1 loop"

FT 118..119 /note= "Dimer interface, at which IL-6R monomers interact
 to form a homodimer"

FT 132..141 /note= "Dimer interface, at which IL-6R monomers interact
 to form a homodimer"

FT 133..138 /note= "L2 loop"

FT 160..168 /note= "L3 loop"

FT 165..169 /note= "SSRY motif"

FT 166..172 /note= "Dimer interface, at which IL-6R monomers interact
 to form a homodimer"

FT 179..196 /note= "Dimer interface, at which IL-6R monomers interact
 to form a homodimer"

FT	/note= "Dimer interface, at which IL-6R monomers interact to form a homodimer"
FT	190..193
FT	/note= "L4 loop"
FT	195..299
FT	/note= "D3 domain"
FT	199..200
FT	/note= "Double proline motif"
FT	226
FT	/note= "N-glycosylated"
FT	227..233
FT	/note= "L5 loop"
FT	227..230
FT	/note= "SSRF motif"
FT	233..239
FT	/label= "Tryptophan-arginine_ladder"
FT	/note= "Forms a left-handed 310 helix structure"
FT	241..250
FT	/note= "Dimer interface, at which IL-6R monomers interact to form a homodimer"
FT	244..248
FT	/label= "Tryptophan-arginine_ladder"
FT	/note= "Forms a left-handed 310 helix structure"
FT	250..256
FT	/note= "L6 loop"
FT	261..262
FT	/note= "Dimer interface, at which IL-6R monomers interact to form a homodimer"
FT	270..290
FT	/label= "Tryptophan-arginine_ladder"
FT	/note= "Forms a left-handed 310 helix structure"
FT	272..276
FT	/note= "Dimer interface, at which IL-6R monomers interact to form a homodimer"
FT	276..281
FT	/note= "L7 loop"
FT	282..290
FT	/note= "Dimer interface, at which IL-6R monomers interact to form a homodimer"
FT	284..287
FT	/note= "WSXWS motif"
FT	302..303
FT	/note= "Double proline motif"
FT	
XX	WO2003025017-A1.
XX	
XX	27-MAR-2003.
XX	
XX	16-SEP-2002; 2002WO-AU001255.
XX	
XX	14-SEP-2001; 2001AU-00007695.
XX	
XX	(GSIR) COMMONWEALTH SCI & IND RES ORG.
XX	(LUDW-) LUDWIG INST CANCER RES.
XX	(HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
XX	
XX	Varghese JN, Simpson RJ, Moritz RL, Lou M, Ji H, Branson KM;
XX	Smith BJ;
XX	WPI; 2003-558820/52.
XX	
XX	Selecting or designing compound interacting with interleukin receptor,
XX	useful for treatment of e.g. AIDS, involves assessing and testing
XX	compound to modulate activity of receptor.
XX	
XX	Disclosure; Page 356-357; 361pp; English.
XX	
XX	The invention relates to selecting or designing a compound that interacts
XX	with the interleukin-6 receptor (IL-6R) via assessing and obtaining the
XX	stereochemical complementarity between the compound and a topographic
XX	region of the receptor and testing the compound for its ability to
XX	modulate an activity associated with the receptor. Also disclosed is the
XX	crystal structure of the IL-6R alpha chain. The compounds of the

Query Match	61.6%	Score 1763;	DB 7;	Length 325;		
Best Local Similarity	100.0%	Pred. No. 7.6e-110;				
Matches 325;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;		
Qy	20	LAPRRCPAQEVARGLVLSBEDSTTLTCPCGVEPBDNATVMHVLAKRPAAGSHPSRWAGMR	79			
Db	1	LAPRRCPAQEVARGLVLSBEDSVTLTCPCGVEPBDNATVMHVLAKRPAAGSHPSRWAGMR	60			
Qy	80	RLILRSVQLHDSGNYSCYRAGRPAQTVHLLVDVPEEPQLSCFRKSPLSNVVCEWGPST	139			
Db	61	RLILRSVQLHDSGNYSCYRAGRPAQTVHLLVDVPEEPQLSCFRKSPLSNVVCEWGPST	120			
Qy	140	PSLTTTKAVLVLRKFNQSPAEDEFOEPCCOYSQESQKFSQCLAVPEGDSFYIVSMCVASSVG	199			
Db	121	PSLTTTKAVLVLRKFNQSPAEDEFOEPCCOYSQESQKFSQCLAVPEGDSFYIVSMCVASSVG	180			
Qy	200	SKESKQTQFCQCGILQDPDPANITVTAVARNPRULSTWQDPHSNNSFFYLRFELRYRA	259			
Db	181	SKFKRTQFQCGILQDPDPANITVTAVARNPRULSTWQDPHSNNSFFYLRFELRYRA	240			
Qy	260	ERSKTFPTTMVKDLOHHCIVHIDAWSGLRHVYQLRAQEEFGQGESEMPKMGTPWTESR	319			
Db	241	ERSKTFPTTMVKDLOHHCIVHIDAWSGLRHVYQLRAQEEFGQGESEMPKMGTPWTESR	300			
Qy	320	SPPAENEVSTPMQALTTNKDDNLL	344			
Db	301	SPPAENEVSTPMQALTTNKDDNLL	325			
RESULT 35						
AAR70122						
ID	AAR70122	standard; protein; 1042 AA.				
XX	XX					
AC	AAR70122;					
XX	XX					
DT	16-OCT-2003 (revised)					
DT	25-MAR-2003 (revised)					
DT	14-FEB-1996 (first entry)					
XX	XX					
DE	IL6-R type 1-GBP 130 fusion protein.					
XX	XX					
KW	Hybrid peptide; malaria parasite; Plasmodium falciparum; fusion protein;					
KW	red blood cell; cytokine receptor; glycophorin binding peptide 130;					
XX	GBP 130; GBPH; glycophorin binding peptide homologue; glycophorin A.					
OS	Homo sapiens.					
OS	Plasmodium falciparum.					
OS	Chimeric.					
XX	XX					
FH	Key	Location/Qualifiers				
FT	Misc-difference 54	/label= OTHER				
FT		/note= "Arn (sic) "				
XX	XX					
PN	W0506737-A1.					
XX	XX					
PD	09-MAR-1995.					
XX	XX					

FT /note= "Double proline motif"
 FT Modified-site 226
 FT /note= "N-glycosylated"
 FT Domain 227..233
 FT /note= "75 loop"
 FT Domain 227..230
 FT /note= "SSPY motif"
 FT Domain 233..239
 FT /label= "Tryptophan-arginine ladder"
 FT /note= "Forms a left-handed 310 helix structure"
 FT Domain 241..250
 FT /note= "Dimer interface, at which IL-6R monomers interact
 FT to form a homodimer"
 FT Domain 244..248
 FT /label= "Tryptophan-arginine ladder"
 FT /note= "Forms a left-handed 310 helix structure"
 FT Domain 250..256
 FT /note= "L6 loop"
 FT Misc-difference 259
 FT /note= "Wild-type Val substituted by Gln"
 FT Domain 261..262
 FT /note= "Dimer interface, at which IL-6R monomers interact
 FT to form a homodimer"
 FT Domain 270..290
 FT /label= "Tryptophan-arginine ladder"
 FT /note= "Forms a left-handed 310 helix structure"
 FT Domain 272..276
 FT /note= "Dimer interface, at which IL-6R monomers interact
 FT to form a homodimer"
 FT Domain 276..281
 FT /note= "L7 loop"
 FT Domain 282..290
 FT /note= "Dimer interface, at which IL-6R monomers interact
 FT to form a homodimer"
 FT Domain 284..287
 FT /note= "MSXWS motif"
 FT Domain 302..303
 FT /note= "Double proline motif"
 PN WO2003025017-A1.
 XX 27-MAR-2003.
 PD 16-SEP-2002; 2002WO-AU001255.
 XX 14-SEP-2001; 2001AU-00007695.
 PR (CSIR) COMMONWEALTH SCI & IND RES ORG.
 XX (LUDWIG INST CANCER RES.
 PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
 PA Varghese JN, Simpson RJ, Moritz RL, Lou M, Ji H, Branson KM,
 PI Smith BJ;
 XX MPI; 2003-558820/52.
 DR Selecting or designing compound interacting with interleukin receptor,
 XX useful for treatment of e.g. AIDS, involves assessing and testing
 PT compound to modulate activity of receptor.
 PT
 XX Example 1; Page; 361pp; English.
 PS
 XX The invention relates to selecting or designing a compound that interacts
 CC with the interleukin-6 receptor (IL-6R) via assessing and obtaining the
 CC stereochemical complementarity between the compound and a topographic
 CC region of the receptor and testing the compound for its ability to
 CC modulate an activity associated with the receptor. Also disclosed is the
 CC crystal structure of the IL-6R alpha chain. The compounds of the
 CC invention act as cytokine receptor modulators and may be useful in the
 CC prevention and treatment of diseases associated with signalling by IL-6R
 CC such as multiple myeloma, lymphoma, inflammation, rheumatoid arthritis,
 CC prostate cancer, Castleman's disease, AIDS, mesangial proliferative
 CC glomerulonephritis, Kaposi's sarcoma, sepsis, osteoporosis and psoriasis.

CC The method provides enhanced stereochemical complementarity relative to
 CC the naturally occurring IL-6 receptor ligand as well as a rational basis
 CC for the development of ligands for specific therapeutic applications. The
 CC information provided by the IL-6R crystal structure will facilitate a
 CC more accurate understanding of how the binding of a ligand leads to
 CC signal transduction. The current sequence is that of the human IL-6R
 CC alpha chain mutant protein of the invention which contains a V259Q
 CC substitution. Note: The present sequence is not shown within the
 CC specification but was created by the indexer using the human IL-6R alpha
 CC chain wild-type protein sequence (AA023014)
 XX
 XX Sequence 325 AA;
 SQ
 Query Match 61.4%; Score 1757; DB 7; Length 325;
 Best Local Similarity 99.7%; Pred. No. 1.9e-109; Indels 0; Gaps 0;
 Matches 324; Conservative 0; Mismatches 1;
 QY 20 LAPRRCPAGEVARGVLTSLPGDSVTLTCGVEPEDNATVHWLKRKPAAGSHPSRMAGMR 79
 DB 1 LAPRRCPAGEVARGVLTSLPGDSVTLTCGVEPEDNATVHWLKRKPAAGSHPSRMAGMR 60
 QY 80 RLLLRVQLHDSGNVSCYRAGRAGTVHLVDYPPPEPOLSCRRKSPLSNVCEMGRPRST 139
 DB 61 RLLLRVQLHDSGNVSCYRAGRAGTVHLVDYPPPEPOLSCRRKSPLSNVCEMGRPRST 120
 QY 140 PSLTTAVLTVKRFQNSPADPEPCQYSEOSQKFCOLAVPEGDSFFYIVSCVASSVG 199
 DB 121 PSLTTAVLTVKRFQNSPADPEPCQYSEOSQKFCOLAVPEGDSFFYIVSCVASSVG 180
 QY 200 SKFSKTQFGCGGIILOPPDPANITTVAVARNPRLSVTQDPHSNNSFFRLRFEILRYRA 259
 DB 181 SKFSKTQFGCGGIILOPPDPANITTVAVARNPRLSVTQDPHSNNSFFRLRFEILRYRA 240
 QY 260 ESKTITTMVWVDLQHHCVIHDAMSGLRVNVQLRADEFGQGSMSSEPMAGTPTTESR 319
 DB 241 ESKTITTMVWVDLQHHCVIHDAMSGLRVNVQLRADEFGQGSMSSEPMAGTPTTESR 300
 QY 320 SPPAENEVSTPMQALTTNKDDNII 344
 DB 301 SPPAENEVSTPMQALTTNKDDNII 325
 RESULT 37
 AA023018
 ID AA023018 standard; protein; 325 AA.
 XX
 AC AA023018;
 XX
 DT 17-SEP-2003 (first entry)
 XX
 XX Human interleukin 6 receptor alpha chain mutant peptide - C192A.
 XX
 XX Cytostatic; antiinflammatory; antirheumatic; antiarthritic; anti-HIV,
 KW nephrotropic; osteoparatic; antipsoriatic; interleukin-6 receptor; IL-6R;
 KW alpha chain; cytokine; multiple myeloma; lymphoma; inflammation; sepsis;
 KW rheumatoid arthritis; prostate cancer; Castleman's disease; AIDS; human;
 KW mesangial proliferative glomerulonephritis; Kaposi's sarcoma; psoriasis;
 KW osteoporosis; protein co-ordinate data; mutant; mutein.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Domain 1..93
 FT /note= "D1 domain"
 FT Domain 1..5
 FT /note= "Dimer interface, at which IL-6R monomers interact
 FT to form a homodimer"
 FT Disulfide-bond 6..174
 FT /label= Disulphide_bond
 FT Domain 19..23
 FT /note= "Dimer interface, at which IL-6R monomers interact
 FT to form a homodimer"

FT Domain 65..69
/note= "Dimer interface, at which IL-6R monomers interact
to form a homodimer"
FT Domain 93..99
/note= "Dimer interface, at which IL-6R monomers interact
to form a homodimer"
FT Domain 94..194
/note= "D2 domain"
FT Domain 94..95
/note= "Double proline motif"
FT Domain 106..110
/note= "L1 loop"
FT Domain 118..119
/note= "Dimer interface, at which IL-6R monomers interact
to form a homodimer"
FT Domain 132..141
/note= "Dimer interface, at which IL-6R monomers interact
to form a homodimer"
FT Domain 133..138
/note= "L2 loop"
FT Domain 160..168
/note= "L3 loop"
FT Domain 165..169
/note= "SSFY motif"
FT Domain 166..172
/note= "Dimer interface, at which IL-6R monomers interact
to form a homodimer"
FT Domain 179..196
/note= "Dimer interface, at which IL-6R monomers interact
to form a homodimer"
FT Domain 190..193
/note= "L4 loop"
FT Misc-difference 192
/note= "Wild-type Cys substituted by Ala"
FT Domain 195..299
/note= "D3 domain"
FT Domain 199..200
/note= "Double proline motif"
FT Modified-site 226
/note= "N-glycosylated"
FT Domain 227..233
/note= "L5 loop"
FT Domain 227..230
/note= "SSFY motif"
FT Domain 233..239
/label= "Tryptophan-arginine ladder
/note= "Forms a left-handed 310 helix structure"
FT Domain 241..250
/note= "Dimer interface, at which IL-6R monomers interact
to form a homodimer"
FT Domain 244..248
/label= "Tryptophan-arginine ladder
/note= "Forms a left-handed 310 helix structure"
FT Domain 250..256
/note= "L6 loop"
FT Domain 261..262
/note= "Dimer interface, at which IL-6R monomers interact
to form a homodimer"
FT Domain 270..290
/label= "Tryptophan-arginine ladder
/note= "Forms a left-handed 310 helix structure"
FT Domain 272..276
/note= "Dimer interface, at which IL-6R monomers interact
to form a homodimer"
FT Domain 276..281
/note= "L7 loop"
FT Domain 282..290
/note= "Dimer interface, at which IL-6R monomers interact
to form a homodimer"
FT Domain 284..287
/note= "MSXMS motif"
FT Domain 302..303
/note= "Double proline motif"

XX WO2003025017-A1.
PN
XX
PD 27-MAR-2003.
XX
PF 16-SEP-2002; 2002WO-AU001255.
XX
PR 14-SEP-2001; 2001AU-00007695.
XX
PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
PA (IUDM-) LUDWIG INST CANCER RES.
PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
PI Varghese JN, Simpson RJ, Moritz RL, Lou M, Ji H, Branson KM,
PI Smith BJ,
XX
DR WPI; 2003-558820/52.
XX
PT Selecting or designing compound interacting with interleukin receptor,
PT useful for treatment of e.g. AIDS, involves assessing and testing
PT compound to modulate activity of receptor.
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PS Example 1; Page; 361pp; English.
XX
CC The invention relates to selecting or designing a compound that interacts
CC with the interleukin-6 receptor (IL-6R) via assessing and obtaining the
CC stereochemical complementarity between the compound and a topographic
CC region of the receptor and testing the compound for its ability to
CC modulate an activity associated with the receptor. Also disclosed is the
CC crystal structure of the IL-6R alpha chain. The compounds of the
CC invention act as cytokine receptor modulators and may be useful in the
CC prevention and treatment of diseases associated with signalling by IL-6R
CC such as multiple myeloma, lymphoma, inflammation, rheumatoid arthritis,
CC prostate cancer, Castleman's disease, AIDS, mesangial proliferative
CC glomerulonephritis, Kaposi's sarcoma, sepsis, osteoporosis and psoriasis.
CC The method provides enhanced stereochemical complementarity relative to
CC the naturally occurring IL-6 receptor ligand as well as a rational basis
CC for the development of ligands for specific therapeutic applications. The
CC information provided by the IL-6R crystal structure will facilitate a
CC more accurate understanding of how the binding of a ligand leads to
CC signal transduction. The current sequence is that of the human IL-6R
CC alpha chain mutant protein of the invention which contains a C192A
CC substitution. Note: The present sequence is not shown within the
CC specification but was created by the indexer using the human IL-6R alpha
CC chain wild-type protein sequence (AA023014)
XX
SQ Sequence 325 Aa;
Query Match 61.3%; Score 1754; DB 7; Length 325;
Best Local Similarity 99.7%; Pred. No. 3.1e-109;
Matches 324; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 20 LARRCPAGRVANGVLTSLPGDSVTLTCGVSEEDNATYMTVLRKPAAGSHPRKMGGR 79
DB 1 LARRCPAGRVANGVLTSLPGDSVTLTCGVSEEDNATYMTVLRKPAAGSHPRKMGGR 60
QY 80 RLILRSVQLHDSNGSYRAGRPAGTWHLLVDVPEEPOLSCRRKSPLSNVCEMGPRST 139
DB 61 RLILRSVQLHDSNGSYRAGRPAGTWHLLVDVPEEPOLSCRRKSPLSNVCEMGPRST 120
QY 140 PSLTTRAVLLVRKFGNSPADPFOECYQSGQSKFCQALVAPGDSFPYIVSMCVASVVG 199
DB 121 PSLTTRAVLLVRKFGNSPADPFOECYQSGQSKFCQALVAPGDSFPYIVSMCVASVVG 180
QY 200 SKFSKTQTFQGGCILLPDPANITTVAVANPNWLSYTTWDDPSNNSSFTRLRPELRRA 259
DB 181 SKFSKTQTFQGGCILLPDPANITTVAVANPNWLSYTTWDDPSNNSSFTRLRPELRRA 240
QY 260 ERSKFTTMMWVKLOHNCVHDAWSGLRHVYVQLRAOEFQCGMSEWSPFAMGTPWTESR 319
DB 241 ERSKFTTMMWVKLOHNCVHDAWSGLRHVYVQLRAOEFQCGMSEWSPFAMGTPWTESR 300
QY 320 SPPEANEVSTPMQALTTNKDDNLL 344

Db 301 SPBAENEVSTPMQALTTNKDDNITL 325

RESULT 38
AAB15389

ID AAB15389 standard; protein; 325 AA.

AC AAB15389;

DT 11-DEC-2000 (first entry)

DE Human interleukin 6 receptor protein.

KM Human: interleukin-6 receptor; fungus; *Pichia pastoris*; PCR primer;

OS Homo sapiens.

FT Misc-difference 57 Location/Qualifiers

FT Misc-difference 281 /note= "encoded by GGC"

FT Misc-difference 281 /note= "encoded by CAA"

PN JP2000157280-A.

PD 13-JUN-2000.

PF 26-NOV-1998; 98JP-00335464.

PR 26-NOV-1998; 98JP-00335464.

PA (TOYO) TOSOH CORP.

DR WPI; 2000-468203/41.

DR N-PSDB; AAA70701.

PT Yeasts transformed with IL-6 receptor gene.

PS Example 1; Page 6-8; 10pp; Japanese.

CC The invention relates to the production of human interleukin-6 receptor (IL-6R) protein in the fungus *Pichia pastoris*. The fungus was transformed with an expression vector (pOIC9-420UL) containing a gene encoding an IL-6R protein having an immunoglobulin-like region and cytokine receptor region and spanning amino acids from Leu20-Ala323. The human IL-6R region was PCR amplified using the primers AAA70702-A70703. This sequence represents the recombinant IL-6R protein of the invention

SO Sequence 325 AA;

Query Match 61.1%; Score 1748; DB 3; Length 325;
Best Local Similarity 99.4%; Pred. No. 7.7e-109;
Matches 323; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 20 LAPRRCPADEVAVAGVLTSLPGDSVTLTCGVEPEDNATVHWLRKPAAGSHPRMAGMGR 79
DB 1 LAPRRCPADEVAVAGVLTSLPGDSVTLTCGVEPEDNATVHWLRKPAAGSHPRMAGMGR 60
QY 80 RLILRSVQLHDSGNVSCYRAGRPAAGTVHLLVDVPEEPOLSCFRKSPLSNVVCEMGPRT 139
DB 61 RLILRSVQLHDSGNVSCYRAGRPAAGTVHLLVDVPEEPOLSCFRKSPLSNVVCEMGPRT 120
QY 140 PSILTTTAVLLVRRKQNSPAEDFOEQYQESQKFSQCLAVPEGDSFFYIVSMCVASSVG 199
DB 121 PSILTTTAVLLVRRKQNSPAEDFOEQYQESQKFSQCLAVPEGDSFFYIVSMCVASSVG 180
QY 200 SKSKSKTQTFQGGCIILOPDPANITVAVANRPMWLSVTWODPHSNWSSFFRLRFEELRYRA 259
DB 181 SKSKSKTQTFQGGCIILOPDPANITVAVANRPMWLSVTWODPHSNWSSFFRLRFEELRYRA 240
QY 260 ERSKFTTMMVVDLOHHCVIHDAMSGLRHVVOQLRAQEEFGQGEWSEMSPEAMGTPWTESR 319

Db 241 ERSKFTTMMVVDLOHHCVIHDAMSGLRHVVOQLRAQEEFGQGEWSEMSPEAMGTPWTESR 300

QY 320 SPBAENEVSTPMQALTTNKDDNITL 344

Db 301 SPBAENEVSTPMQALTTNKDDNITL 325

RESULT 39

AAB15390

ID AAB15390 standard; protein; 325 AA.

AC AAB15390;

DT 15-DEC-2000 (first entry)

DE Bovine interleukin-12 p35 subunit protein.

KM Antifective; bovine; interleukin 12; IL12; heterodimer; infection.

OS Bos taurus.

PN JP2000157274-A.

PD 13-JUN-2000.

PF 20-NOV-1998; 98JP-00331052.

PR 20-NOV-1998; 98JP-00331052.

PA (DAUC) DAICHI PHARM CO LTD.

DR WPI; 2000-468201/41.

DR N-PSDB; AAA70708.

PT Preparation of bovine interleukin 12 comprising using a vector containing the gene encoding it, useful for the prevention and treatment of chronic and opportunistic infections.

PS Example 1; Page 8; 11pp; Japanese.

CC The invention relates to a method for the preparation of bovine interleukin 12 (BoIL12). BoIL12 consists of a heterodimer of p35 and p40 subunits. BoIL12 is produced by introducing into a host cell recombinant vectors containing genes encoding the p35 and p40 subunits. This sequence represents the bovine IL12 p35 subunit. Interleukin 12 is used for the prevention and treatment of chronic infections and opportunistic infections

SO Sequence 325 AA;

Query Match 61.1%; Score 1748; DB 3; Length 325;
Best Local Similarity 99.4%; Pred. No. 7.7e-109;
Matches 323; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 20 LAPRRCPADEVAVAGVLTSLPGDSVTLTCGVEPEDNATVHWLRKPAAGSHPRMAGMGR 79
DB 1 LAPRRCPADEVAVAGVLTSLPGDSVTLTCGVEPEDNATVHWLRKPAAGSHPRMAGMGR 60
QY 80 RLILRSVQLHDSGNVSCYRAGRPAAGTVHLLVDVPEEPOLSCFRKSPLSNVVCEMGPRT 139
DB 61 RLILRSVQLHDSGNVSCYRAGRPAAGTVHLLVDVPEEPOLSCFRKSPLSNVVCEMGPRT 120
QY 140 PSILTTTAVLLVRRKQNSPAEDFOEQYQESQKFSQCLAVPEGDSFFYIVSMCVASSVG 199
DB 121 PSILTTTAVLLVRRKQNSPAEDFOEQYQESQKFSQCLAVPEGDSFFYIVSMCVASSVG 180
QY 200 SKSKSKTQTFQGGCIILOPDPANITVAVANRPMWLSVTWODPHSNWSSFFRLRFEELRYRA 259
DB 181 SKSKSKTQTFQGGCIILOPDPANITVAVANRPMWLSVTWODPHSNWSSFFRLRFEELRYRA 240
QY 260 ERSKFTTMMVVDLOHHCVIHDAMSGLRHVVOQLRAQEEFGQGEWSEMSPEAMGTPWTESR 319

CC The method provides enhanced stereochemical complementarity relative to
CC the naturally occurring IL-6 receptor ligand as well as a rational basis
CC for the development of ligands for specific therapeutic applications. The
CC information provided by the IL-6 crystal structure will facilitate a
CC more accurate understanding of how the binding of a ligand leads to
CC signal transduction. The current sequence is that of the human IL-6R
CC alpha chain mutant protein of the invention which contains a W214N
CC substitution. Note: The present sequence is not shown within the
CC specification but was created by the indexer using the human IL-6R alpha
CC chain wild-type protein sequence (AA023014)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 9, 2004, 08:55:07 ; Search time 47.8543 seconds
(without alignments)
1091.766 Million cell updates/sec

Title: US-09-462-416-7
Perfect score: 2861
Sequence: 1 MNAVCAALALALAAAGAL.....LILRSFKETLQSLRLRQW 543

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1918	67.0	468	1 A41242	interleukin-6 rece
2	954.5	33.4	460	2 JL0144	interleukin-6 rece
3	954.5	33.4	460	2 JL0145	interleukin-6 rece
4	938.5	32.8	212	1 IVHDB2	interleukin-6 prec
5	853	29.8	462	1 A37986	interleukin-6 rece
6	571.5	20.0	208	2 T09216	interleukin-6 prec
7	559.5	19.6	212	2 I46621	prointerleukin 6 -
8	557.5	19.5	212	2 I46590	interleukin 6 - pi
9	476	16.6	207	1 A56610	interleukin 6 - ca
10	471	16.5	208	1 A56610	interleukin-6 prec
11	465	16.3	208	1 S29549	interleukin-6 - sh
12	396.5	13.9	211	2 A34247	interleukin-6 prec
13	374.5	13.1	211	1 ICM66	interleukin-6 prec
14	337	11.8	432	2 I48343	interleukin-11 rec
15	330.5	11.6	422	2 I37891	interleukin-11 rec
16	310	10.8	372	2 I58141	ciliary neurotroph
17	306.5	10.7	362	2 S60614	growth promoting a
18	301	10.5	372	1 UHHUON	ciliary neurotroph
19	226	7.9	53	2 I53394	soluble interleuk
20	198.5	6.9	328	2 A38957	interleukin 12b pr
21	180	6.3	21	2 J01655	prolactin receptor
22	178.5	6.2	830	2 I50455	prolactin receptor
23	171	6.0	2	2 I45971	prolactin receptor
24	167.5	5.9	917	2 I49699	glycoprotein 130 -
25	167.5	5.9	2	2 A36337	membrane glycoprot
26	166	5.8	918	2 A44257	interleukin-6 sign
27	161.5	5.6	616	2 A30304	prolactin receptor
28	159	5.6	310	2 A29884	prolactin receptor
29	159	5.6	412	2 A41070	prolactin receptor

30	159	5.6	610	2 A34631	lactogen receptor
31	159	5.6	610	2 A36116	prolactin receptor
32	158.5	5.5	335	2 I27899	interleukin 12 p40
33	158	5.5	630	2 I51086	prolactin receptor
34	155	5.4	292	2 I77525	prolactin receptor
35	155	5.4	303	2 I77524	prolactin receptor
36	155	5.4	608	2 I53269	prolactin receptor
37	146	5.1	890	1 A53743	protein-tyrosine k
38	144	5.0	1896	2 T08851	Down syndrome cell
39	138	4.8	288	2 B59405	prolactin receptor
40	138	4.8	376	2 A59405	prolactin receptor
41	138	4.8	622	2 A40144	prolactin receptor
42	137.5	4.8	882	2 I36912	receptor tyrosine
43	134.5	4.7	895	2 S74225	leptin receptor, 1
44	133.5	4.7	837	2 A34898	granulocyte colony
45	133.5	4.7	880	1 J04166	protein-tyrosine k

ALIGNMENTS

RESULT 1

A41242
Interleukin-6 receptor precursor - human
N:Contains: interleukin-6 receptor, soluble form
C:Species: Homo sapiens (man)
C>Date: 27-Mar-1992 #sequence revision 02-Dec-1994 #text_change 09-Jul-2004
C:Accession: A41242; J00080; S17468; A61459; S14621
R:Yamasaki, K.; Taga, T.; Hirata, Y.; Yawata, H.; Kawashita, Y.; Seed, B.; Taniguchi, T.;
Science 241, 825-828, 1988
A:Title: Cloning and expression of the human interleukin-6 (BSF-2/IFNbeta 2) receptor.
A:Reference number: A41242; MUID:88305347; PMID:3136546
A:Accession: A41242
A:Molecule type: mRNA
A:Residues: 1-468 <YAM>
A:Cross-references: UNIPROT:P08887; GB:M20566; NID:G33845; PID:CAA31312.1; PID:G33846
R:Yamasaki, K.; Taga, T.; Hirata, Y.; Yawata, H.; Kawashita, Y.; Seed, B.; Taniguchi, T.;
Proc. Jpn. Acad. 64, 209-211, 1988
A:Title: Molecular structure of interleukin 6 receptor.
A:Reference number: J00080
A:Accession: J00080
A:Molecule type: mRNA
A:Residues: 1-468 <YAM>
A:Cross-references: EMBL:X58298; NID:G32580; PID:CAA41231.1; PID:G32581
A:Experimental source: heptoma cell line HepG2
R:Novick, D.; Engelmann, H.; Wallach, D.; Rubinstein, M.
J. Exp. Med. 170, 1409-1414, 1989
A:Title: Soluble cytokine receptors are present in normal human urine.
A:Reference number: A61459; MUID:90010793; PMID:2529343
A:Accession: A61459
A:Molecule type: protein
A:Residues: 20-49 <NOV>
C:Comment: Through this receptor, interleukin-6 induces proliferation, activation, and d
C:Comment: This growth factor receptor does not have a tyrosine kinase domain.
C:Genetics:
A:Gene: GDB:IL6R
A:Cross-references: GDB:127966; OMIM:147880
A:Map position: 1921-1921
C:Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immunog
C:Keywords: acute phase; cytokine receptor; glycoprotein; transmembrane protein
F:1-19/Domain: signal sequence #status predicted <Sig>
F:20-468/Product: interleukin-6 receptor #status predicted <Ext>
F:20-363/Domain: extracellular #status predicted <Ext>
F:40-98/Domain: immunoglobulin homology <IMW2>
F:121-309/Domain: cytokine receptor homology <CRS>
F:364-386/Domain: transmembrane #status predicted <TMW>

F:387-468/Domain: intracellular #status predicted <INT>
F:47-96/Disulfide bonds: #status predicted
F:55,93,221,245,350/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 67.0%; Score 1918; DB 1; Length 468;
Best Local Similarity 96.5%; Pred. No. 2,8e-125;
Matches 360; Conservative 1; Mismatches 4; Indels 8; Gaps 1;

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QY 1 MLAVGALLAALAAAGALAPRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATYTM 60
DB 1 MLAVGALLAALAAAGALAPRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATYTM 60
QY 61 VLKRPAGSHPRWAGMGRRLILRSVOLHDSGNVSCYRAGRPAQVHLVDPPEEPQLS 120
DB 61 VLKRPAGSHPRWAGMGRRLILRSVOLHDSGNVSCYRAGRPAQVHLVDPPEEPQLS 120
QY 121 CFRKSPLSNVCEMGPSTPSLTITKAVLLVRKFONSPAEDPOEPOYSQESQKFSQCLAV 180
DB 121 CFRKSPLSNVCEMGPSTPSLTITKAVLLVRKFONSPAEDPOEPOYSQESQKFSQCLAV 180
QY 181 PEGDSSFYIVSMCVASVSGSKSKTQTFQGGIILQPDPPANITVTAVARNPRMLSVTMOD 240
DB 181 PEGDSSFYIVSMCVASVSGSKSKTQTFQGGIILQPDPPANITVTAVARNPRMLSVTMOD 240
QY 241 PHSNMSFFYRLRFEELRYAERSKTTTMMVVDLQHCYIHDAMSGLRHVQLRAQEEFQG 300
DB 241 PHSNMSFFYRLRFEELRYAERSKTTTMMVVDLQHCYIHDAMSGLRHVQLRAQEEFQG 300
QY 301 GEMSWSEPMAGTPTESRSPAPENESTPMQALITNKDDNLIIFRDSANATSLPYEF 360
DB 301 GEMSWSEPMAGTPTESRSPAPENESTPMQALITNKDDNLIIFRDSANATSLPYEF 360
QY 361 VPGEDESKDVAAAP 373
DB 357 ----QDSSSVLP 365

```

RESULT 2

Interleukin-6 receptor precursor (clone lambda p1) - mouse
C/Species: Mus musculus (house mouse)
C/Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C/Accession: J10144
R/Sugita, T.; Torioka, T.; Saito, M.; Yamasaki, K.; Taga, T.; Hirano, T.; Kishimoto, T.
J. Exp. Med. 171, 2001-2009, 1990
A/Title: Functional murine interleukin 6 receptor with the intracisternal a particle gen
A/Reference number: J10144; MUID:90278354; PMID:2112585
A/Accession: J10144
A/Status: nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-440 <SUG>
A/Cross-references: UNIPROT:P22272; GB:X51976; NID:953548; PIDN:CAA36238.1; PID:953549
C/Keywords: cytokine receptor; transmembrane protein
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-440/Product: interleukin-6 receptor #status predicted <SIG>
F:40-94/Domain: immunoglobulin homology <IMM>
F:117-306/Domain: cytokine receptor homology <CRS>
F:358-385/Domain: transmembrane #status predicted <TRA>

Query Match 33.4%; Score 954.5; DB 2; Length 440;
Best Local Similarity 50.1%; Pred. No. 1.5e-58;
Matches 188; Conservative 52; Mismatches 122; Indels 13; Gaps 5;

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QY 1 MLAVGALLAALAAAGALAPRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATYTM 60
DB 1 MLAVGCTLLVALAALAAVAVLVLGSCRALREAVANGTVSLPGATVTLCPGKEAAGNVTIHW 60
QY 61 VLKRPAGSHPRWAGMGRRLILRSVOLHDSGNVSCYRAGRPAQVHLVDPPEEPQLS 120
DB 61 VLKRPAGSHPRWAGMGRRLILRSVOLHDSGNVSCYRAGRPAQVHLVDPPEEPQLS 120
QY 121 CFRKSPLSNVCEMGPSTPSLTITKAVLLVRKFONSPAEDPOEPOYSQESQKFSQCLAV 180
DB 121 CFRKSPLSNVCEMGPSTPSLTITKAVLLVRKFONSPAEDPOEPOYSQESQKFSQCLAV 180
QY 181 PEGDSSFYIVSMCVASVSGSKSKTQTFQGGIILQPDPPANITVTAVARNPRMLSVTMOD 240
DB 181 PEGDSSFYIVSMCVASVSGSKSKTQTFQGGIILQPDPPANITVTAVARNPRMLSVTMOD 240
QY 241 PHSNMSFFYRLRFEELRYAERSKTTTMMVVDLQHCYIHDAMSGLRHVQLRAQEEFQG 300
DB 241 PHSNMSFFYRLRFEELRYAERSKTTTMMVVDLQHCYIHDAMSGLRHVQLRAQEEFQG 300
QY 301 GEMSWSEPMAGTPTESRSPAPENESTPMQALITNKDDNLIIFRDSANATSLPYEF 360
DB 301 GEMSWSEPMAGTPTESRSPAPENESTPMQALITNKDDNLIIFRDSANATSLPYEF 360
QY 361 VPGEDESKDVAAAP 373
DB 357 ----QDSSSVLP 365

```

Interleukin-6 receptor precursor (clone lambda 301) - mouse
C/Species: Mus musculus (house mouse)
C/Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C/Accession: J10145; S14543
R/Sugita, T.; Torioka, T.; Saito, M.; Yamasaki, K.; Taga, T.; Hirano, T.; Kishimoto, T.
J. Exp. Med. 171, 2001-2009, 1990
A/Title: Functional murine interleukin 6 receptor with the intracisternal a particle gene
A/Reference number: J10144; MUID:90278354; PMID:2112585
A/Accession: J10145
A/Status: nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-460 <SUG>
A/Cross-references: UNIPROT:P22272; GB:X51975; NID:949725; PIDN:CAA36237.1; PID:949726
A/Experimental source: clone lambda 301
R/Fiorillo, M.T.; Ciliberto, G.; Dente, L.
submitted to the EMBL data library, July 1990
A/Description: Cloning and expression of murine IL-6 receptor.
A/Reference number: S14543
A/Accession: S14543
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-373, 'R', 375-460 <PIO>
A/Cross-references: EMBL:X53802; NID:952692; PIDN:CAA37810.1; PID:952693
C/Keywords: cytokine receptor; transmembrane protein
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-460/Product: interleukin-6 receptor #status predicted <SIG>
F:40-94/Domain: immunoglobulin homology <IMM>
F:117-306/Domain: cytokine receptor homology <CRS>
F:358-385/Domain: transmembrane #status predicted <TRA>

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QY 117 CFRKSPLSNVCEMGPSTPSLTITKAVLLVRKFONSPAEDPOEPOYSQESQKFSQCLAV 176
DB 117 CFRKSPLSNVCEMGPSTPSLTITKAVLLVRKFONSPAEDPOEPOYSQESQKFSQCLAV 176
QY 180 VPGEDESKDVAAAP 373
DB 180 VPGEDESKDVAAAP 373
QY 241 PHSNMSFFYRLRFEELRYAERSKTTTMMVVDLQHCYIHDAMSGLRHVQLRAQEEFQG 300
DB 241 PHSNMSFFYRLRFEELRYAERSKTTTMMVVDLQHCYIHDAMSGLRHVQLRAQEEFQG 300
QY 300 GEMSWSEPMAGTPTESRSPAPENESTPMQALITNKDDNLIIFRDSANATSLPYEF 358
DB 297 LGQMSWSEPMAGTPTESRSPAPENESTPMQALITNKDDNLIIFRDSANATSLPYEF 351
QY 359 MPVPGEDESKDVAAAP 373
DB 352 --LAPVQESSMSLP 364

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RESULT 3

Interleukin-6 receptor precursor (clone lambda 301) - mouse
C/Species: Mus musculus (house mouse)
C/Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C/Accession: J10145; S14543
R/Sugita, T.; Torioka, T.; Saito, M.; Yamasaki, K.; Taga, T.; Hirano, T.; Kishimoto, T.
J. Exp. Med. 171, 2001-2009, 1990
A/Title: Functional murine interleukin 6 receptor with the intracisternal a particle gene
A/Reference number: J10144; MUID:90278354; PMID:2112585
A/Accession: J10145
A/Status: nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-460 <SUG>
A/Cross-references: UNIPROT:P22272; GB:X51975; NID:949725; PIDN:CAA36237.1; PID:949726
A/Experimental source: clone lambda 301
R/Fiorillo, M.T.; Ciliberto, G.; Dente, L.
submitted to the EMBL data library, July 1990
A/Description: Cloning and expression of murine IL-6 receptor.
A/Reference number: S14543
A/Accession: S14543
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-373, 'R', 375-460 <PIO>
A/Cross-references: EMBL:X53802; NID:952692; PIDN:CAA37810.1; PID:952693
C/Keywords: cytokine receptor; transmembrane protein
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-460/Product: interleukin-6 receptor #status predicted <SIG>
F:40-94/Domain: immunoglobulin homology <IMM>
F:117-306/Domain: cytokine receptor homology <CRS>
F:358-385/Domain: transmembrane #status predicted <TRA>

Query Match 33.4%; Score 954.5; DB 2; Length 460;
Best Local Similarity 50.1%; Pred. No. 1.6e-58;
Matches 188; Conservative 52; Mismatches 122; Indels 13; Gaps 5;

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QY 1 MLAVGALLAALAAAGALAPRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATYTM 60
DB 1 MLAVGCTLLVALAALAAVAVLVLGSCRALREAVANGTVSLPGATVTLCPGKEAAGNVTIHW 60
QY 61 VLKRPAGSHPRWAGMGRRLILRSVOLHDSGNVSCYRAGRPAQVHLVDPPEEPQLS 120
DB 61 VLKRPAGSHPRWAGMGRRLILRSVOLHDSGNVSCYRAGRPAQVHLVDPPEEPQLS 120
QY 121 CFRKSPLSNVCEMGPSTPSLTITKAVLLVRKFONSPAEDPOEPOYSQESQKFSQCLAV 179
DB 121 CFRKSPLSNVCEMGPSTPSLTITKAVLLVRKFONSPAEDPOEPOYSQESQKFSQCLAV 176
QY 180 VPGEDESKDVAAAP 373
DB 180 VPGEDESKDVAAAP 373
QY 241 PHSNMSFFYRLRFEELRYAERSKTTTMMVVDLQHCYIHDAMSGLRHVQLRAQEEFQG 300
DB 241 PHSNMSFFYRLRFEELRYAERSKTTTMMVVDLQHCYIHDAMSGLRHVQLRAQEEFQG 300
QY 300 GEMSWSEPMAGTPTESRSPAPENESTPMQALITNKDDNLIIFRDSANATSLPYEF 358
DB 297 LGQMSWSEPMAGTPTESRSPAPENESTPMQALITNKDDNLIIFRDSANATSLPYEF 351
QY 359 MPVPGEDESKDVAAAP 373
DB 352 --LAPVQESSMSLP 364

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QY 240 DPHSNNSFFYRLFEFLRYPAERSKTFTTMMVKDLQHHCVIHDAMSGLRHVOLRAQEEFG 299
 DB 237 HETWDPSTYLLQFOFARYFPVWSKERTVLLLPVAVQOCYIHDLRKRVKVVQVGRKEEID 296
 QY 300 QCEWSEWSEPMAGTQM-TESRSPPAENEVSTPMQALTTKKDDNIIIFRDSANATSLPVEF 358
 DB 297 LQWSEWSEWSEVGTGTPWIAPIPRRTTPA-GILMNPQVSVESDANHEDDYESSTEXTSV---- 351
 QY 359 MEVPPEDESKDVAAAP 373
 DB 352 --LAPVQESSWSLSP 364

RESULT 4
 IYHUB2
 Interleukin-6 precursor [validated] - human
 N/Alternate names: B-cell differentiation factor; B-cell hybridoma growth factor; B-cell
 on factor
 C/Species: Homo sapiens (man)
 C/Date: 28-Dec-1987 #sequence revision 28-Dec-1987 #text change 09-Jul-2004
 C/Accession: A32648; A25692; A26966; A33515; A25801; A25921; I52193; I56003; A27601; B27
 R;Ishikawa, K.; Hirano, T.; Watanabe, Y.; Muratani, K.; Matsuda, T.; Nakai, S.; Kishimoto
 EMBO J. 6, 2939-2945, 1987
 A/Title: Structure and expression of human B cell stimulatory factor-2 (BSF-2/IL-6) gene
 A/Reference number: A32648; PMID:88082664; PMID:3500852
 A/Accession: A32648
 A/Molecule type: DNA
 A/Residues: 1-212 <YAS>
 A/Cross-references: UNIPROT:P05231; GB:X00081; NID:G29494; PIDN:CAA68278.1; PID:G29495
 A/Note: the authors translated the codon CAG for residue 130 as Glu
 R;Zilberstein, A.; Ruggieri, R.; Korn, J.H.; Revel, M.
 EMBO J. 5, 2529-2537, 1986
 A/Title: Structure and expression of cDNA and genes for human interferon-beta-2, a direct
 A/Reference number: A91051; PMID:87053818; PMID:3023045
 A/Accession: A25692
 A/Molecule type: mRNA
 A/Residues: 1-212 <ZIL>
 A/Cross-references: GB:X04430; NID:G32673; PIDN:CAA28026.1; PID:G32674
 R;Hirano, T.; Yasukawa, K.; Harada, H.; Taga, T.; Watanabe, Y.; Matsuda, T.; Kashimura
 I. T.; Kishimoto, T.
 Nature 344, 73-76, 1986
 A/Title: Complementary DNA for a novel human interleukin (BSF-2) that induces B lymphocy
 A/Reference number: A93387; PMID:87065033; PMID:3491322
 A/Accession: A26966
 A/Molecule type: mRNA
 A/Residues: 1-212 <HIR>
 A/Cross-references: GB:X04602; NID:G33849; PIDN:CAA28268.1; PID:G33850
 R;Tonouchi, N.; Miwa, K.; Karsanuyama, H.; Matsui, H.
 Biochem. Biophys. Res. Commun. 163, 1056-1062, 1989
 A/Title: Deletion of 3' untranslated region of human BSF-2 mRNA causes stablization of
 A/Reference number: A33515; PMID:89391958; PMID:2789513
 A/Accession: A33515
 A/Molecule type: mRNA
 A/Residues: 1-212 <TON>
 A/Cross-references: GB:M29150; NID:G186349; PIDN:AAA59154.1; PID:G307063
 R;Haeghebaert, G.; Content, J.; Volckaert, G.; Derynck, R.; Tavernier, J.; Fiers, W.
 Eur. J. Biochem. 159, 625-632, 1986
 A/Title: Structural analysis of the sequence coding for an inducible 26-kDa protein in h
 A/Reference number: A25801; PMID:87004683; PMID:3758081
 A/Accession: A25801
 A/Molecule type: DNA; mRNA
 A/Residues: 1-212 <HAE>
 A/Cross-references: GB:X04403
 A/Experimental source: fibroblast
 R;May, L.T.; Helfgott, D.C.; Sehgal, P.B.
 Proc. Natl. Acad. Sci. U.S.A. 83, 8957-8961, 1986
 A/Title: Anti-beta-interferon antibodies inhibit the increased expression of HLA-B7 mRNA
 A/Reference number: A25921; PMID:87067433; PMID:3538015
 A/Accession: A25921
 A/Molecule type: mRNA
 A/Residues: 1-212 <NAV>
 A/Cross-references: GB:M14584; NID:G184628; PIDN:AAA52728.1; PID:G306910
 R;Wong, G.G.; Witek-Giannotti, J.; Hewick, R.M.; Clark, S.C.; Ogawa, M.

Behring Inst. Mitt. 83, 40-47, 1988
 A/Title: Interleukin 6: identification as a hematopoietic colony-stimulating factor.
 A/Reference number: I52193; PMID:89193317; PMID:3266663
 A/Accession: I52193
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-212 <MON>
 A/Cross-references: GB:M54894; NID:G186351; PIDN:AA41704.1; PID:G186352
 R;Brakenhoff, J.P.; de Groot, E.R.; Evers, R.F.; Pannekoek, H.; Aarden, L.A.
 J. Immunol. 139, 4116-4121, 1987
 A/Title: Molecular cloning and expression of hybridoma growth factor in Escherichia coli.
 A/Reference number: I56003; PMID:88088768; PMID:3320204
 A/Accession: I56003
 A/Status: translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-212 <BRA>
 A/Cross-references: GB:M18403; NID:G184631; PIDN:AAA52729.1; PID:G306911
 R;Van Damme, J.; Van Beeumen, J.; Decock, B.; Van Snick, J.; De Ley, M.; Billiau, A.
 J. Immunol. 140, 1534-1541, 1988
 A/Title: Separation and comparison of two monokines with lymphocyte-activating factor act
 A/Reference number: A92816; PMID:88154445; PMID:3279116
 A/Accession: A27601
 A/Molecule type: protein
 A/Residues: 28-51; 'X', 53-57, 'X', 59, 'X', 61 <VAN1>
 A/Accession: B27601
 A/Molecule type: protein
 A/Residues: 30-56, 'XX', 59-61, 'X', 63 <VA2>
 R;Yamamoto, R.; Lin, L.S.; Lowe, R.; Warren, M.K.; White, T.J.
 J. Immunol. 144, 1808-1816, 1990
 A/Title: The human lung fibroblast cell line, MRC-5, produces multiple factors involved v
 A/Reference number: A60400; PMID:90171574; PMID:2307841
 A/Accession: A60400
 A/Molecule type: protein
 A/Residues: 29-42 <HIR2>
 R;Hirano, T.; Taga, T.; Yasukawa, K.; Nakajima, K.; Nakano, N.; Takatsuki, F.; Shimizu, A
 Proc. Natl. Acad. Sci. U.S.A. 84, 228-231, 1987
 A/Title: Human beta-cell differentiation factor defined by an anti-peptide antibody and
 A/Reference number: A29085; PMID:87092370; PMID:3491991
 A/Accession: A29085
 A/Molecule type: protein
 A/Residues: 29-42 <HIR2>
 R;Node, M.; Takekura, K.; Sugimoto, H.; Hosoi, T.; Takechi, K.; Hara, T.; Ishikawa, H.; Ar
 Anticancer Res. 11, 961-968, 1991
 A/Title: Purification and characterization of human fibroblast derived differentiation fa
 A/Reference number: A61159; PMID:91290785; PMID:1648338
 A/Accession: A61159
 A/Molecule type: protein
 A/Residues: 30-42 <NOD>
 A/Experimental source: fibroblast
 R;Wing, J.E.; Carnetti, C.; Steinman, R.M.; Granelli-Pigerno, A.
 J. Mol. Cell. Immunol. 4, 203-212, 1989
 A/Title: Interleukin 6 is the principal cytokine T lymphocyte differentiation factor for
 A/Reference number: A61462; PMID:90121567; PMID:2610854
 A/Accession: A61462
 A/Molecule type: protein
 A/Residues: 28-48 <MIN>
 A/Experimental source: leukocyte-conditioned medium
 R;May, L.T.; Shaw, J.E.; Khanna, A.K.; Zdzienicka, J.B.; Sehgal, P.B.
 Cytokine 3, 204-211, 1991
 A/Title: Marked cell-type-specific differences in glycosylation of human interleukin-6.
 A/Reference number: A48419; PMID:91355644; PMID:1883960
 A/Accession: A48419
 A/Molecule type: protein
 A/Residues: 30-37, 'X', 39-40 <NAV2>
 A/Experimental source: FS-4 fibroblasts
 A/Note: sequence extracted from NCBI backbone
 A/Note: this 28-30K form contained both N-linked and O-linked carbohydrate; a 25K form cc
 A/Accession: C48419
 A/Molecule type: protein
 A/Residues: 28-40 <NAV3>
 A/Experimental source: FS-4 fibroblasts
 A/Note: sequence extracted from NCBI backbone (NCBIP:63787)
 A/Note: this 23-25K form contained O-linked but not N-linked carbohydrate

R;Orlita, T.; Oheda, M.; Hasegawa, M.; Kubonlwa, H.; Esaki, K.; Ochi, N.
 J. Biochem. 115, 345-350, 1994
 A>Title: Polypeptide and carbohydrate structure of recombinant human interleukin-6 prod
 A:Reference number: JX0305; MUID:94266765; PMID:8206884
 A:Contents: annotation; modified sites in recombinant protein from CHO cells
 R;Clogston, C.L.; Boone, T.C.; Crandall, C.; Mendiaz, E.A.; Lu, H.S.
 Arch. Biochem. Biophys. 272, 144-151, 1999
 A>Title: Disulfide structures of human interleukin-6 are similar to those of human granu
 A:Reference number: S04981; MUID:69286115; PMID:2472117
 A:Contents: annotation; disulfide bonds in recombinant protein
 R;Rock, F.L.; Li, X.; Cheng, P.; Ida, N.; Klein, M.
 Biochemistry 33, 5146-5154, 1994
 A>Title: Roles of disulfide bonds in recombinant human interleukin 6 conformation.
 A:Reference number: A54253; MUID:94227044; PMID:8172889
 A:Contents: annotation; lability and functional significance of each disulfide bond
 C;Comment: Produced by both lymphoid and nonlymphoid tissue in response to growth factor
 C;Comment: This protein plays a regulatory role in various host defense mechanisms and e
 C;Genetics:
 A;Gene: GDB:116
 A;Cross-references: GDB:120748; OMIM:147620
 A;Map position: 7p21-7p21
 A;Intons: 7/1; 70/3; 108/3; 157/3
 C;Superfamily: interleukin 6
 C;Keywords: Castleman's disease; cytokine; extracellular protein; glycoprotein; growth f
 F;1-27/Domain: signal sequence #status predicted <SIG>
 F;28-212/Product: interleukin-6, long form #status experimental <MATL>
 F;30-212/Product: interleukin-6, short form #status experimental <MATS>
 F;72-78,101-111/Disulfide bonds: #status experimental
 F;73/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental
 F;166/Binding site: carbohydrate (Thr) (covalent) (partial) #status experimental
 F;172/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 32.8%; Score 938.5; DB 1; Length 212;
 Best Local Similarity 97.9%; Pred. No. 7.2e-58;
 Matches 187; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 354 LPVEF-MVPPEGDSKVAAPHROPLTSSSRIDKQIRYIIDGISALRKETCNKSNMCESS 412
 Db 22 LPAAFPAPVPPEGDSKVAAPHROPLTSSSRIDKQIRYIIDGISALRKETCNKSNMCESS 81

QY 413 KEALAENNNLTPKAAEKDGFQSGFNEETCLVKITITGLLEFEVYLETLOQRFSSSEQAR 472
 Db 82 KEALAENNNLTPKAAEKDGFQSGFNEETCLVKITITGLLEFEVYLETLOQRFSSSEQAR 141

QY 473 AVOMSTKVLIOPLQKAKNDAITTPDPTTNASLITGLQAOQONWLODMTHLILRSKPEF 532
 Db 142 AVOMSTKVLIOPLQKAKNDAITTPDPTTNASLITGLQAOQONWLODMTHLILRSKPEF 201

QY 533 LQSSSLRALROM 543
 Db 202 LQSSSLRALROM 212

RESULT 5
 A37986
 Interleukin-6 receptor precursor - rat
 N:Alternate names: IL-6 receptor
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
 C/Accession: A37986
 R;Baumann, M.; Baumann, H.; Fey, G.H.
 J. Biol. Chem. 265, 19853-19862, 1990
 A>Title: Molecular cloning, characterization and functional expression of the rat liver
 A:Reference number: A37986; MUID:91060602; PMID:2174054
 A:Accession: A37986
 A:Molecule type: mRNA
 A:Residues: 1-462 <BAT>
 A:Cross-references: UNIPROT:P22273; GB:MS8587; GB:J05668; NID:g204921; PIDN:AAA41431.1;
 C;Comment: After binding IL-6, this chain associates with a 130k glycoprotein that is es
 C;Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immunog
 C;Keywords: acute phase; cytokine receptor; transmembrane protein
 F;1-19/Domain: signal sequence #status predicted <SIG>

F;20-462/Product: interleukin-6 receptor #status predicted <MAT>
 F;20-362/Domain: extracellular #status predicted <EXT>
 F;40-99/Domain: immunoglobulin homology <IMM>
 F;117-306/Domain: cytokine receptor homology <CRS>
 F;363-385/Domain: transmembrane #status predicted <TM>
 F;386-462/Domain: intracellular #status predicted <INT>
 F;47-92/Disulfide bonds: #status predicted

Query Match 29.8%; Score 853; DB 1; Length 462;
 Best Local Similarity 48.4%; Pred. No. 1.7e-51;
 Matches 181; Conservative 50; Mismatches 119; Indels 24; Gaps 8;

QY 1 MLAVGALIAALIAAPGALAPRCPAOPAVGLTSPGDSVTLLCPGPEEDNATVAM 60
 Db 1 MLAVGTLVALLAARAVALLVSGCALEVANGVTSLPGAVITLCPKEAAGNATTIM 60

QY 61 VLKRPAGSHPSRWAGMRRLILRSYQLHDSGNYCYRAGRAGVTHLIVDPPEBPQS 120
 Db 61 VY----SGSQSRWMTTGNITLVLRVAVQVNDTGHYLCFLDDHVGTVPLIVDPPEBPQS 116

QY 121 CPKKSPLSNVCEWGRSPSLITTKAVILLVRKQNSPAE-DROEPQYQSQKSPSCOLA 179
 Db 117 CPKKNPLVNAFCBMHSPSTPSTTKAVMFAKKINTNGSKDPQVPCQYSQQLKSPSCVEE 176

QY 180 VPEGDSFYIVAMCVASVSGSKFKTQTPQGGGIILOPDPANITVAVARN-----PR 232
 Db 177 ILEGDKVHYIVGLCVANVSIGSRSHNVVQSLKMTQVDPDPALVVASLIGSLVGSKSVGK 236

QY 233 WLSTVWQDPHSMNNGSYRLRFELRLRAERSKFTTMMVKDLOHRCVTHDAMGSLRHVQL 292
 Db 237 TISPQTQVTTCCNSPDDTLYGQ-----FTFWPPLQVAOHQCVIHDLALGVKHVVQV 289

QY 293 RAQEEFGQSGMSPEAMGTPM-TESRSPAPNEVSTPMQALTTNKDDNLTLPDSANA 351
 Db 290 RQKEEFDIQMSKMBEVTGTPLAEPRTTPA-GIPGNPTQVSVDYDHEQDQSSSTBA 348

QY 352 TSL--PVE-FMVP 362
 Db 349 TSVLAPVQGSSPIP 362

RESULT 6
 T09216
 Interleukin-6 precursor - horse
 C:Species: Equus caballus (domestic horse)
 C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
 C/Accession: T09216
 R;Swiderski, C.E.; Horohov, D.W.
 submitted to the EMBL Data Library, July 1996
 A:Reference number: Z16613
 A:Accession: T09216
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-208 <SWI>
 A:Cross-references: UNIPROT:Q95181; EMBL:U64794; NID:g2654387; PID:g2654388
 C;Genetics:
 A;Gene: IL-6
 C;Superfamily: interleukin-6
 C;Keywords: cytokine; growth factor

Query Match 20.0%; Score 571.5; DB 2; Length 208;
 Best Local Similarity 58.5%; Pred. No. 1.9e-32;
 Matches 113; Conservative 32; Mismatches 41; Indels 7; Gaps 3;

QY 351 APLSPVEFMPVPPEGDSKVAAPHROPLTSSSRIDKQIRYIIDGISALRKETCNKSNMCESS 410
 Db 23 APLSPF---PLPLGDETTSSNGP--LITPADKTKQHIKYLIGKISALNKENCNPFSSCKE 76

QY 411 SSKKALAENNNLTPKAAEKDGFQSGFNEETCLVKITITGLLEFEVYLETLOQRFSSSEQ 470
 Db 77 NKVEYLAENNNLTPKAAEKDGFQSGFNEETCLVKITITGLLEFEVYLETLOQRFSSSEQ 136

QY 471 ARAVOMSTKVLIOPLQKAKNDAITTPDPTTNASLITGLQAOQONWLODMTHLILRSKPEF 530

[illegible]

RESULT 11
S29549
Interleukin-6 - sheep
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: S29549
R:Ebrahimi, B.
submitted to the EMBL Data Library, October 1992
A:Reference number: S29549
A:Accession: S29549
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-208 <ERR>
A:Cross-references: UNIPROT:P29455; EMBL:X68723
C:Superfamily: Interleukin-6

	Query Match	16.3%	Score 465;	DB 1;	Length 208;
	Best Local Similarity	50.5%;	Pred. No.	4.5e-25;	
	Matches	92;	Conservative	34;	Mismatches 52; Indels 4; Gaps 2
Oy	360	PVPGEDSKDVAAHPROPFTSSERLDQIIRYLDIGISALRKETCNKSNMCSSKEALAEN	419		
Dd	29	PPPLLEDFNDPTTPSLILITTEPKETBALKHIVDKISAIRKEICEKNDECEKNSKETLAEN	88		
Oy	420	NINLPRMAEKDCGFOSGFEWERTCYVKTITGLIEFEFYLYEYLQNRFESSSEQARVMSTK	479		
Dd	89	KIKIPMEKKDCGFOSGFQAACLLIKTTAGLLEYOYIDFLONFEEGNDETWELOSSTR	148		
Oy	480	VLIIOFLCKAKKNIIDAITPDPPTTNASILTRLOAQNOMILODMTHILLRSFKETLOSSRA	539		
Dd	149	TIIQIILKEKIAGL--ITT--PAITHDLEKMQSNEWMNAKVITILRSLLENPLORCLRA	204		
Oy	540	LR 541			
Dd	205	IR 206			

RESULT 12
A34247
Interleukin-6 precursor - rat
N:Alternate names: IL-6
C:Species: Rattus norvegicus (Norway rat)
C:Date: 15-Jun-1990 #sequence_revision 15-Jun-1990 #text_change 09-Jul-2004
C:Accession: A34247
R:Northemann, W.; Braciak, T.A.; Hattori, M.; Lee, F.; Fey, G.H.
J. Biol. Chem. 264, 16072-16082, 1989
A:Title: Structure of the rat interleukin 6 gene and its expression in macrophage-derive
A:Reference number: A34247; WUID:89380206; PMID:2789217
A:Accession: A34247
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-211 <MOR>

A;Cross-references: UNIPROT:P20607, GB:M26744; NID:g204915; PIND:AAA77659.1; PID:g204916
C;Superfamily: Interleukin-6
C;Keywords: cytokine; growth factor; immunoregulation; lymphokine; macrophage

Query Match 13.9%; Score 396.5; DB 2; Length 211;
Best Local Similarity 39.4%; Pred. No. 2.5e-20;
Matches 76; Conservative 53; Mismatches 59; Indels 5; Gaps 3;

QY 351 ATSTPVEEMPVPGDSKDVAFPHROPLTSSRIDKQIYYLIGDISALRKETCNKSMCE 410
 |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||:
DB 22 AIAFPTS-QVRGDFTEDT--HHRPVYTTSQVGLITYLVREILIMRELGNAGSDCM 77
 |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||:
QY 411 SSKELAENNINLPYMAEKDGFOSGEENBETCLAVKITTLGLEFEVLLEYIQNPF-ESSE 469
 ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||:
DB 78 NSDDDLSENINLTLPFIORNDGCFGTGVNQEICLTKCSGLLERFYELEFYKNMLQDKKD 137
 :|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||:
QY 470 QARAVMSQKVLIQFLQKKAKMIDLATTDPPTNASLLITKLQAQNOMQLDMTHLLIRSF 529
 ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||:
CSubsuperfamily 138 KRVIVQSNETLVHI FKQEI KD SYK I V L P T P S N A L M E K L E S O K W I R T K T I O L I L K A L 197

QY 530 KEFLQSLRALRQ 542
 :|||::|||::|||:
DB 198 EEFLKYVMSTRQ 210

RESULT 13
 ICMS6
 Interleukin-6 precursor - mouse
 N:Alternate names: B-cell hybridoma growth factor; B-cell stimulating factor 2; hepatocyte
 acytoma growth factor
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Jun-1990 #sequence revision 30-Jun-1990 #ext change 09-Jul-2004
 C:Accession: A30531, A27610, A30571, S01323, S12103, E34047, A26662, A40486, A60799, S107
 R:Rabinbe, O.; Altira, S.; Kamaya, T.; Wong, G.G.; Hirano, T.; Kishimoto, T.
 J. Immunol. 141, 3875-3881, 1988
 A:Title: Genomic structure of the murine IL-6 gene. High degree conservation of potential
 A:Reference number: A30531, MUID:89035525, PMID:3263439
 A:Accession: A30531
 A:Molecule type: DNA
 A:Residues: 1-211 <RAN>
 A:Cross-references: UNIPROT:P08505; GB:M20572; NID:g198369; PIDN:AA39302.1; PID:g387386
 R:Van Snick, J.; Cayphas, S.; Szlikora, J.P.; Renaud, J.C.; Van Roost, E.; Boon, T.; Simy
 Eur. J. Immunol. 18, 193-197, 1988
 A:Title: cDNA cloning of murine interleukin-Hp1: homology with human interleukin 6.
 A:Reference number: A27610, MUID:8816883; PMID:2965020
 A:Accession: A27610
 A:Molecule type: mRNA
 A:Residues: 1-211 <VAN>
 A:Cross-references: GB:X06203; NID:g52701; PIDN:CAA29560.1; PID:g527202
 R:Mock, B.A.; Nordam, R.P.; Justice, M.J.; Kozak, C.; Jenkine, N.A.; Copeland, N.G.; Cla
 J. Immunol. 142, 1372-1376, 1989
 A:Title: The murine IL-6 gene maps to the proximal region of chromosome 5.
 A:Reference number: A30571, MUID:89124383; PMID:2563387
 A:Accession: A30571
 A:Molecule type: mRNA
 A:Residues: 5-211 <MOC>
 A:Cross-references: GB:R24221; NID:g341131; PIDN:AAA68814.1; PID:g870699
 R:Stimpson, R.J.; Moritz, R.L.; Rubira, M.R.; Van Snick, J.
 Eur. J. Biochem. 176, 187-197, 1988
 A:Title: Murine hybridoma/plasmacytoma growth factor. Complete amino-acid sequence and re
 A:Reference number: S01323, MUID:88329053; PMID:3262055
 A:Accession: S01323
 A:Molecule type: protein
 A:Residues: 25-166 'X', 168-211 <SIM>
 A:Note: the sequence from Fig. 11 is inconsistent with that from Fig. 10 in having 103-Aa
 R:Grenett, H.E.; Fuentes, N.L.; Fuller, G.M.
 Nucleic Acids Res. 18, 6455, 1990
 A:Title: Cloning and sequence analysis of the cDNA for murine interleukin-6.
 A:Reference number: S12103, MUID:91057159; PMID:2243807
 A:Accession: S12103
 A:Molecule type: mRNA
 A:Residues: 1-211 <GRE>
 A:Cross-references: EMBL:X54542; NID:g52727; PIDN:CAA3411.1; PID:g52728

R.Jahnen, W.; Ward, L.D.; Reid, G.E.; Moritz, R.L.; Simpson, R.J.
 Biochem. Biophys. Res. Commun. 167: 139-145, 1990
 A:Title: Internal amino acid sequencing of procleins by in situ cyanogen bromide cleavage
 A:Reference number: A90157; NCID:90147651; PMID:2302197
 A:Accession: E34047
 A:Molecule type: protein
 A:Residues: 66-69, 'X', 71-75, 78-94, 128-148 <JAS>
 R:Van Snick, J.; Cayphas, S.; Vink, A.; Uytendhoeve, C.; Coulie, P.G.; Rubira, M.R.; Simpf
 Proc. Natl. Acad. Sci. U.S.A. 83: 9679-9683, 1986
 A:Title: Purification and NH2-terminal amino acid sequence of a T-cell-derived lymphokin
 A:Reference number: A26662; NCID:87092311; PMID:2948184
 A:Accession: A26662
 A:Molecule type: protein
 A:Residues: 25-39, 'X', 41-42, 'X', 44-45 <VSN>
 R:Chiu, C.P.; Mould, C.; Coffman, R.L.; Remick, D.; Lee, F.
 Proc. Natl. Acad. Sci. U.S.A. 85: 7039-7103, 1988
 A:Title: Multiple biological activities are expressed by a mouse interleukin 6 cDNA clone
 A:Reference number: A40486; NCID:89017145; PMID:3262872
 A:Accession: A40486
 A:Molecule type: mRNA
 A:Residues: 1-211 <CHI>
 A:Cross-references: GB:J03783; NCID:919367; PID:AAA39301.1; PID:9309410
 R:Shabo, Y.; Locem, J.; Rudinstein, M.; Revel, M.; Clark, S.C.; Wolf, S.F.; Kamen, R.; S
 Blood 72, 2070-2073, 1988
 A:Title: The myeloid blood cell differentiation-inducing protein MGI-2A is interleukin-6
 A:Reference number: A60799; NCID:89062753; PMID:3264198
 A:Accession: A60799
 A:Molecule type: protein
 A:Residues: 77-98 <SHA>
 R:Blakestein, T.; Qin, Z.; Li, W.; Diamantstein, T.
 J. Exp. Med. 171, 965-970, 1990
 A:Title: DNA rearrangement and constitutive expression of the interleukin 6 gene in a m
 A:Reference number: S10241; NCID:90171860; PMID:2106569
 A:Accession: S10241
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-6 <BLA>
 A:Cross-references: EMBL:X51457; NCID:949738; PID:CAA35824.1; PID:9581860
 R:Zhang, J.G.; Reid, G.E.; Moritz, R.L.; Ward, L.D.; Simpson, R.J.
 Eur. J. Biochem. 217, 53-59, 1993
 A:Title: Specific covalent modification of the cryptophan residues in murine interleukin
 A:Reference number: S38254; NCID:94039075; PMID:8223586
 A:Accession: S38254
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 38-60/75, 'X', 77-79, 176-203 <ZHA>
 C:Genetics:
 A:Gene: 11-6
 A:Map position: 5
 A:Introns: 7/1; 68/3; 106/3; 156/3
 C:Superfamily: interleukin-6
 C:Keywords: Castleman's disease; cytokine; growth factor; immunoregulation; lymphokine;
 F:1-24/Domain: signal sequence #status predicted <SIG>
 F:25-211/Product: interleukin-6 #status experimental <MAT>

Query Match	13.1%	Score 374.5;	DB 1;	Length 211;
Best Local Similarity	39.6%	Pred. No. 8.5e-19;		
Matches	76;	Conservative 49;	Mismatches 62;	Indels 5;
			Gaps 4;	
QY	352	TSHPVFMFPPGDSKDVAAPRROPITSERIDKQIRYLIDGIALRKETCKSNWCS	411	
DB	23	TAFPTTS-QVRRDPTED-TTPNR-PVYTTISQVGLITHVLMETVEMKELCNGNDCA	78	
QY	412	SKEALENNINLPKMAKDCGCFOSGNETCLVYITGLIEFEVYLEYQNR-ESSEQ	470	
DB	79	NDALENNINLPKLEIQRNDCGYOTGYNOEICLKISSGLEHYHSYLEYMNKNKDKK	138	
QY	471	ARAVOMSTKYLIOFLQKKAQNLATTPDPTNASLITKQAQNMOMQDTHLLISPK	530	
DB	139	ARVLQMDTELTILINQOEVKDLHKIVLPISNALLTDKLSQKEMLRKTIOFILKSL	198	
QY	531	EFLQSSLRALRQ	542	

DB 199 EFLKVTINSTRQ 210
 RESULT 14
 148343
 Interleukin-11 receptor alpha-chain precursor - mouse
 N:Alternate names: cytokine type 1 receptor
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
 C:Accession: I48343; S51619
 R:Neuhaus, H.; Bettenhausen, B.; Bilinski, P.; Simon-Chazottes, D.; Guenet, J.L.; Gossler
 Dev. Biol. 166, 521-542, 1994
 A:Title: et12, a novel putative type-1 cytokine receptor expressed during mouse embryoge
 A:Reference number: I48343
 A:Accession: I48343
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-432 <RES>
 A:Cross-references: UNIPROT:O64385; EMBL:X74953; NCID:9673437; PID:CAA52908.1; PID:967343
 R:Hilton, D.J.; Hilton, A.A.; Ratclic, A.; Rakar, S.; Harrison-Smith, M.; Gough, N.M.; E
 EMBO J. 13, 4765-4775, 1994
 A:Title: Cloning of a murine IL-11 receptor alpha-chain; requirement for gp130 for high
 A:Reference number: S51619; NCID:95045367; PMID:7957045
 A:Accession: S51619
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-432 <HIL>
 A:Cross-references: EMBL:U14412; NCID:9576454; PID:AAA53248.1; PID:9576455
 C:Genetics:
 A:Gene: Et12/Il11
 C:Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; [immunog]
 C:Keywords: cytokine receptor
 F:120-310/Domain: cytokine receptor homology <CRS>

Query Match	11.8%	Score 337;	DB 2;	Length 432;
Best Local Similarity	28.0%	Pred. No. 8.7e-16;		
Matches	115;	Conservative 52;	Mismatches 165;	Indels 78;
			Gaps 17;	
QY	2	LAVGCALLAALAAPAL--APRCRAQVARGVITSLPGSVTLTCGPVEDNATVH	59	
DB	1	MSSSCSGLRVLVAAVATLVSSSPCPQAWGPGVQGGPRVWLCCPGV-----	51	
QY	60	WTLRKPAAGSHPSRW-----AGMRLLLRVQLHDSGNYCYRA-GRPAGT	105	
DB	52	-----SAGT-PVSNFRDDSDRLQCPDGLHRLVLAQVDPDETTYCQTLIDVSGGM	104	
QY	106	VHLVDVPEEPQSLCFRKSPLSNVVCWGPSTPSLTAKAVLVKRFQNSPAEDFOE--	163	
DB	105	VTLKGLFPARPPEVSC-QAVDYENFSCWSPQVSGLPFRVLTYSRKTLPGAESQRES	163	
QY	164	-----PCOYSQSSQKSCQLAVPEGDS--SFYIVSNCAVSSGSKSKTQTOGC-----	211	
DB	164	STGPPWC-----PQDPLEASRCVHGAEFWSBYRINTEVNPJGA-----STCLDVR	211	
QY	212	--GILODPANITVAVARNPRLSVTWQDPHSW--NSGFYRLFELRAERSKFTTM	268	
DB	212	LSILRPDPQIGRVSVCYTRRLASTYTPASMRQGHFLKFLQIRPAQHPMST--	270	
QY	269	MYXDLOHNCVHDAMSGLRHVYQLRAQEPFGGGEWSPEAMGTPTESRSPAPANEVS	328	
DB	271	--VEPIGLEBIVTDAVAVLHRAVRSARDPLDAGTWSAPFAMGTRST-----GFLDDEI-	324	
QY	329	TMQALITTKKDDNILFRDSANATSLPVFEMFPPGDSKDVAAPRROP	378	
DB	325	-PDWSQHQQQLAAVAQDSPAARP-SLQDPPRLD-----HRDPL	365	

RESULT 15
 137891
 Interleukin-11 receptor alpha chain - human
 C:Species: Homo sapiens (man)
 C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
 C:Accession: I37891; G01970;

R:Cherel, M.; Sorel, M.; Lebeau, B.; Dubois, S.; Moreau, J.F.; Bataille, R.; Minvielle, B. Blood 86, 2534-2540, 1995
 A:Title: Molecular cloning of two isoforms of a receptor for the human hematopoietic cytokine IL-3
 A:Reference number: 137891, MUID:95399754; PMID:7670098
 A:Accession: 137891
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-422 <RES>
 A:Cross-references: UNIPROT:Q16542; EMBL:Z38102; NID:995653; PIDD:CAAB6224.1; PID:995653
 R:Van Leuven, F. EMBL Data Library, July 1995
 submitted to the EMBL Data Library, July 1995
 A:Reference number: G08959
 A:Accession: G01970
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-422 <VAN>
 A:Cross-references: EMBL:U32323; NID:9975334; PIDD:AA36492.1; PID:9975335
 R:Van Leuven, F. submitted to the EMBL Data Library, July 1995
 A:Reference number: G08961
 A:Accession: G01971
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-422 <VA2>
 A:Cross-references: EMBL:U32324; NID:9975336; PIDD:AA36492.1; PID:9975337
 C:Genetics: A:Insertions: 34/1; 54/2; 111/1; 149/2; 160/2; 216/1; 270/3; 318/1; 358/1; 390/2; 418/1
 C:Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immunoglobulin domain; cytokine receptor homology <CRS>
 F:120-310/Domain: cytokine receptor homology <CRS>
 Query Match 11.6%; Score 330.5; DB 2; Length 422;
 Best Local Similarity 28.9%; Pred. No. 2.4e-15;
 Matches 112; Conservative 46; Mismatches 174; Indels 53; Gaps 15;
 QY 2 LANGCAGLALAAAPGAL--APRCRPAQEVARGVLTSLPGDSVTLTCPEVEPEDNATVH 59
 DB 1 MSSSCGSLRYLVAVATALVASSPCPQAMGPVGQYQGPGRSVKCCPGVTAGD--PVS 58
 QY 60 W-----VLRKPAAGSHPRMAGMRLLRSVQLHDSGNVSCYRA--GRPACTVHLVD 111
 DB 59 WFRDGEKTLQGPD-----SGLGHVLAQADSTDEGTYYICQTLDAIGATVTLQDG 110
 QY 112 VPPEPQLSCFRKPSLNVVCEWGPSTPSLT-----KAVLVKRFQNSPAEDFOE 163
 DB 111 YPPARPVVSC-QADYENFSCWSPQISGLPTRYLTSYRKKTLYGADSGRRSSTG-PW 168
 QY 164 PCQYSGESQKFSQCLAVPBGDS--SFYIVMCVASSVGSFKSTQTQFGCGIILQPPAN 221
 DB 169 PC----PQDPLGAARCVVHGAEFWSQYRINVTENVPGLAS--TRLLDVSLQSIILRPDPQG 223
 QY 222 ITTAVARNPRMLSVTWQDPHSWN--SSFYRLRFELRYRAERSKFTTMMVKDLOHCVIH 280
 DB 224 LRVESVGYPRRLRASTYTPASWPCQPHFLKFLQYRPAOHAMSTVEPAGLEB--VIT 281
 QY 281 DAVSGLHVYQLRAQEEFGQEGSEMSPEAMGTPTWTS-----RSPPAENEVS 328
 DB 282 DAVAGLHAHVARSARDPLDAGTWSTWSPBAMGTSTGTIPKEIRPAMQGLHQPVEPQVD 341
 QY 329 TTPMALITNKDDNITL-FRDSANATSL 354
 DB 342 SPAPRPSPLOPHRPLDHRDSVEQVAV 368
 RESULT 16
 158141
 ciliary neurotrophic factor receptor alpha chain - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
 C:Accession: 158141; A47387
 R:IP, N.Y.; McClain, J.; Barreuzeta, N.X.; Aldrich, T.H.; Pan, L.; Li, Y.; Wiegand, S.T. Neuron 10, 89-102, 1993
 A:Title: The alpha component of the CNTF receptor is required for signaling and defines A:Reference number: 158141; MUID:93152175; PMID:8318290

A:Accession: 158141
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-372 <IPN>
 A:Cross-references: UNIPROT:Q08406; GB:S54212; NID:g265055; PIDD:AA25290.1; PID:g265056
 R:Clatterbuck, R.E.; Price, D.L.; Koliatsos, V.E. Proc. Natl. Acad. Sci. U.S.A. 90, 2222-2226, 1993
 A:Title: Ciliary neurotrophic factor prevents retrograde neuronal death in the adult cent A:Reference number: A47387; MUID:93211934; PMID:8460125
 A:Accession: A47387
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 185-260, 'D', 262-277 <CLA>
 A:Cross-references: GB:S57711; NID:g299331; PIDD:AA25918.1; PID:g299332
 A:Experimental source: Sprague-Dawley, brain
 A>Note: sequence extracted from NCBI backbone (NCBI:128471, NCBI:P128472)
 C:Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immunoglobulin domain; cytokine receptor homology <CRS>
 F:116-296/Domain: cytokine receptor homology <CRS>
 Query Match 10.8%; Score 310; DB 2; Length 372;
 Best Local Similarity 29.8%; Pred. No. 5.3e-14;
 Matches 113; Conservative 46; Mismatches 146; Indels 74; Gaps 17;
 QY 11 ALTAAPGALAAAPRCRPAQEVARGVLTSLPGDSVTLTCPEVEPEDNATVHVLKPPAAGSH 70
 DB 11 AVTAAAAAAYVYQKSHPQE-APHYQYERIGDTVTLPC-GTASMD-AAVTVRVN-----GTD 63
 QY 71 PSRWAGMRLLRSVQLHDSGNVSCYR--AGRPACTVHLVDVPPPEPQLSCFRKSPIS 128
 DB 64 IADDLNGSLQILRSIELHSGISGLYACFHRDWMRLRQVLLHGLPREPVLSCRSNTYRK 123
 QY 129 NVVCEW---GPRSTBLTKAVLVKRF---QNSPAEDQEPQYQSGESQKFSQCLAVPE 182
 DB 124 GFYCSMHLNAPYIYPTFNTVTLHSGKMMVCEKDP-----LKRCHIRYMH 170
 QY 183 GDSSF-YIVMCVASSVGSFKSTQTQFGCGIILQPPANITVAVARNPRMLSVTWQDP 241
 DB 171 LFTITKXKYSISVSNMLGNH-TTATFDEFTIYKPPFENVAVRPVSPNRRLEVTWQTF 229
 QY 242 HSW-NSSFYRLRFLRYRAERSKFTTMMVKDLOHHC-----YIHDAWSGLRVQL 292
 DB 230 STWPDESPFLKFLFYRP-----LILDMQVHLSNGTAHTITDAVAKEYYIQV 280
 QY 293 RAGEFGQEGSEMSPEAMGTPTWTSRSPPAENEVTPMALITNKDDNITLFRDSANAT 352
 DB 281 AARDN-ELGTWSDMSVAHAHTPTER---PRHITTEAQAPE-----TT 320
 QY 353 SLPEFEMPVP-----PGE 365
 DB 321 STTSSLAPEPTTKICDPGE 339
 RESULT 17
 S60614
 growth promoting activity receptor alpha precursor - chicken
 C:Species: Gallus gallus (chicken)
 C>Date: 27-Apr-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
 C:Accession: S60614
 R:Heiler, S.; Finn, T.P.; Huber, J.; Nishi, R.; Geissen, M.; Pieschel, A.W.; Rohrer, H. Development 121, 2681-2693, 1995
 A:Title: Analysis of function and expression of the chick GPA receptor (GPRA1pha) suggests A:Reference number: S60614; MUID:95401882; PMID:7671828
 A:Accession: S60614
 A>Status: preliminary; nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-362 <HEH>
 A:Cross-references: UNIPROT:P51641; EMBL:Z48168; NID:9974147; PIDD:CAAB8184.1; PID:930633
 C:Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immunoglobulin domain; cytokine receptor homology <CRS>
 F:114-294/Domain: cytokine receptor homology <CRS>

Query Match 10.7%; Score 306.5; DB 2; Length 362;
 Best Local Similarity 29.4%; Pred. No. 8, 9e-14;
 Matches 100; Conservative 47; Mismatches 128; Indels 65; Gaps 16;

QY 40 GDSVTLTCGVEPEDNATVHWLVRKPAAG-----SHPSRWAGGRLLRSVOLHDSQNY 94
 DB 37 GADVTMKCGSMDMD--AAVTWT-----ANGTIDIDSHLN-----GSYLILKNDVLTQSGQY 85
 QY 95 SCTYRAG--RPACTVHLVDPPEEPQLSCFRKSPLSNVCEWGRPRSTPLTKAVILVVK 152
 DB 86 SCYEGSSWHLKXQYTLRVGVPPPEVPLMKRSNNYPKGYCSW---HLPGPT-----YIPNS 138
 QY 153 FQNSPAEDFOEPQOYQESQKSCQALAVEGDSF-YIVSMCVASVGSKFSKTQFGQC 211
 DB 139 FVISTYIHGRENVCEKDITPKRCHIRYQLSTVYKXKTLVYTNALG-KNSTLTITDFDF 197
 QY 212 GILQDPDPANITVTAVARNPRLSVTMDPHSW-NSSFYRLRPELRRAERSKTFITMVV 270
 DB 198 ALVKEDPPESVYAKPVNNPRLEVSWQNPSSWPDSPFLKPFLLKRRP-----LI 248
 QY 271 KQLQHHK-----YIHANSGLRHVQQLRAQEEGQESKESPEAMGTPTESRSP 322
 DB 249 LDQWQHVELSDGTSHTITDAVAGKEYIIVAAKDN-DIGTWSMVSVAVHATPWTE- 303
 QY 323 AENEVSTPMQALTTNKDDNILLFRDSANATSLPVEFMPVP 362
 DB 304 -PKHLTEVQITET-----TSTST--STMPPP 328

RESULT 18

UHHUCN

ciliary neurotrophic factor receptor alpha precursor - human
 N:Alternate names: CNTF receptor
 C:Species: Homo sapiens (man)
 C>Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
 C/Accession: A40854; A56526
 R:Davis, S.; Aldrich, T.H.; Valenzuela, D.M.; Wong, V.; Furch, M.E.; Squinto, S.P.; Yanc
 Science 253, 59-63, 1991
 A>Title: The receptor for ciliary neurotrophic factor.
 A/Reference number: A40854; MUID:91289158; PMID:1648265
 A/Accession: A40854
 A:Molecule type: mRNA
 A:Residues: 1-372 <DNA>
 A/Cross-references: UNIPROT:P26992; GB:M73238
 R:Valenzuela, D.M.; Rojas, E.; Le Beau, M.M.; Espinosa III, R.; Braman, C.I.; McClain,
 Genomics 25, 157-163, 1995
 A>Title: Genomic organization and chromosomal localization of the human and mouse genes
 A/Reference number: A56526; MUID:95293367; PMID:7774913
 A/Accession: A56526
 A:Molecule type: DNA
 A:Residues: 1-346, S', 348-372 <VAL>
 A/Cross-references: GB:L38025; NID:9608654; PIDN:AAA91337.1; PID:9608656
 C/Comment: The CNTF receptor is attached to the membrane by a glycosylphosphatidylinositol
 C/Comment: The CNTF receptor sequence appears to contain several PEST regions.
 C/Genetics:
 A:Gene: GDB:CNTR
 A/Cross-references: GDB:134652; OMIM:118946
 A:Map position: 9p13-9p13
 C/Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immunog
 C/Keywords: glycoprotein; growth factor receptor; membrane protein; phosphatidylinositol
 F:1-20/Domains: signal sequence #status predicted <SIG>
 F:21-372/Product: ciliary neurotrophic factor receptor #status predicted <MAT>
 F:39-91/Domains: immunoglobulin homology <IMM>
 F:116-296/Domains: cytokine receptor homology <CRS>
 F:46-89/Disulfide Bonds: #status predicted
 F:60,70,142,190/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 10.5%; Score 301; DB 1; Length 372;
 Best Local Similarity 29.2%; Pred. No. 2, 2e-13;
 Matches 112; Conservative 44; Mismatches 150; Indels 78; Gaps 18;

QY 6 CALLAALAPGAAALAPRCAPQAVARGVLTSLPGDSVTLTCGVEPEDNATVHWLVRK 65

DB 10 CAVLA---AAAAVVAAQRHSPOE--APHVQERLSDVTLPC-GRANMD-AAVTRVFN-- 60
 QY 66 AAGSHPSRWAGGRLLRSVOLHDSQNYSCYR--AGRAGVHLLVDPPEEPQLSCFR 123
 DB 61 --GTLADPLDLNGSQLVHGLGELGSHGLYACHRDSWHLRHQVLLHVGJLPPPEVPLVSCS 118
 QY 124 KSPLSNVCEW---GPRSTPSLTTRKAVLLVRK---QNSPADFOEPQOYQESQKFSQ 177
 DB 119 NTYPKGFYSWHLPTPTYPNTFNFTVHGSIMCEQDA-----LKNRCH 165
 QY 178 LAVEGDSF-YIVSMCVASVGSKFSKTQFGGIIQDPDPANITVTAVARNPRLSV 236
 DB 166 IRYMLFSTIKYKVSISVNALGHN-ATATDEFTIVKPDDEPNVAVAPSPNPRLEV 224
 QY 237 TWQDPHSW-NSSFYRLRPELRRAERSKTFITMWKDLQHC-----YIHDMSGLR 287
 DB 225 TWQTSWPDPSFPLKFLRYRP-----LILDQWQHVELSDGTAHTTDAVAGKE 275
 QY 288 HVVQLRQAEFGQESKESPEAMGTPTESRSPANEVSTPMQALTTNKDDNILLFRD 347
 DB 276 YIIQVAAKDN-EIGTWSMVSVAHATPWTE-----PRULTTEAQAAET----- 318
 QY 348 SANATSLPVEFMPVP-----PGE 365
 DB 319 ---TSTTSSLAAPPPTTKICDPGE 339

RESULT 19

I53394

Soluble interleukin-6 receptor - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
 C/Accession: I53394
 R:Horluch, S.; Koyanagi, Y.; Zhou, Y.; Miyamoto, H.; Tanaka, Y.; Waki, M.; Matsumoto, A.
 Eur. J. Immunol. 24, 1945-1948, 1994
 A>Title: Soluble interleukin-6 receptors released from T cell or granulocyte/macrophage

A/Reference number: I53394; MUID:94333499; PMID:8056053
 A/Accession: I53394
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-53 <RES>
 A/Cross-references: GB:S72848; NID:9633862; PIDN:AAC60635.1; PID:9633863
 C/Genetics:
 A:Gene: IL6-GR
 C/Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immunog
 C/Keywords: cytokine receptor

Query Match 7.9%; Score 226; DB 2; Length 53;
 Best Local Similarity 100.0%; Pred. No. 2, 6e-09;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 313 TPWTSRSPPAENEVSTPMQALTTNKDDNILLFRDSANATSLP 355
 DB 1 TPWTSRSPPAENEVSTPMQALTTNKDDNILLFRDSANATSLP 43

RESULT 20

A38957

interleukin 12B precursor [validated] - human
 N:Alternate names: cytotoxic lymphocyte maturation factor 40X chain; natural killer cell
 C:Species: Homo sapiens (man)
 C/Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
 C/Accession: A38957; B39359; S21688; B36055
 R:Wolfe, S.F.; Temple, P.A.; Kobayashi, M.; Young, D.; Diczig, M.; Lowe, L.; Dzialo, R.; Fj
 J. Immunol. 146, 3074-3081, 1991
 A>Title: Cloning of cDNA for natural killer cell stimulatory factor, a heterodimeric cytc
 A/Reference number: A38957; MUID:91201875; PMID:1673147
 A/Accession: A38957
 A:Molecule type: mRNA
 A:Residues: 1-328 <WOL>

Query Match 7.9%; Score 226; DB 2; Length 53;
 Best Local Similarity 100.0%; Pred. No. 2, 6e-09;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 313 TPWTSRSPPAENEVSTPMQALTTNKDDNILLFRDSANATSLP 355
 DB 1 TPWTSRSPPAENEVSTPMQALTTNKDDNILLFRDSANATSLP 43

A;Cross-references: UNIPROT:P29460; GB:M65290
R;Gibler, U.; Chua, A.O.; Schoenhaut, D.S.; Dwyer, C.M.; McComas, W.; Motyka, R.; Nabavi
Proc. Natl. Acad. Sci. U.S.A. 88, 4143-4147, 1991
A;Title: Coexpression of two distinct genes is required to generate secreted bioactive c
A;Reference number: A39359; MUID:91235523; PMID:1674604
A;Accession: B39359
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-328 <GB>
A;Cross-references: GB:M65272; GB:M38444; NID:g180625; P1DN:AAA35695.1; P1D:g180626
Arch. Biochem. Biophys. 294, 230-237, 1992
A;Title: Molecular characterization of interleukin 12.
A;Reference number: S21688; MUID:92198015; PMID:11347984
A;Accession: S21688
A;Molecule type: protein
A;Residues: 23-28;46-59;74-80, 'X', 94-130;161-169, 'X', 171-180;213-235;240-250;289-299, 'X'
A;Experimental source: lymphoblastoid cell line NC-37
R;Stern, A.S.; Podlaski, F.J.; Hulmes, J.D.; Pan, Y.C.E.; Quinn, P.M.; Wolitzky, A.G.; F
Proc. Natl. Acad. Sci. U.S.A. 87, 6808-6812, 1990
A;Title: Purification to homogeneity and partial characterization of cytotoxic lymphocy
A;Reference number: A36055; MUID:90370873; PMID:2204066
A;Accession: B36055
A;Molecule type: protein
A;Residues: 23-45 <STE>
A;Experimental source: lymphoblastoid cell line NC-37
C;Genetics:
A;Gene: GDB:IL12B; NKSF2
A;Cross-references: GDB:127870; OMIM:161561
A;Map position: 5q31.1-5q33.1
C;Keywords: cytokine; glycoprotein; heparin binding; heterodimer
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-328/Product: interleukin 12B #status predicted <MAT>
F;27-30/Region: heparin binding #status predicted
F;125/Binding site: carbohydrate (Asn) (covalent) #status absent
F;135-303/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;222/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;319/Modified site: 2'-mannosyl-tryptophan (TTP) (partial) #status experimental

Query Match 6.9%; Score 198.5; DB 2; Length 328;
Best Local Similarity 24.1%; Pred. No. 2,4e-06;
Matches 81; Conservative 51; Mismatches 135; Indels 69; Gaps 14;
QY 13 LAAPGAAALRRCPADVANGVLTSLPGDSVLTTCPCGEEDENATYMWLVRKPAAGSHPS 72
Db 16 LAAPLVAIMELKXDVVVELDWPDAEGEMVLTCDPPE-EDGIT- -WTL- - - - -DQSS 66
QY 73 RWAGMRRLILRSVQLHDSGNSCYRAGRAGTVHLLV- - - - -DV- - - - -PPEE 116
Db 67 EVLGGKTLTYQKEFGDAGQVYCHKGGEVLSHLLHKKEDGIWSTDILKDKQKPKK 126
QY 117 POLSCFRKPLSNVNCVEM- - - - -GPRSTPLTTKAVLVRKFGNSPAD 160
Db 127 TFLRCEKKNVSGFCTCMWLTITDITLFSYKSSRGSSDPQGVTCGAATLSAEVRGDNKE 186
QY 161 FQPCQYQSGESQFSCQLAVPEDSSFYIYVSCVAVSGSKFQTKTQFGCGILQDPPEA 220
Db 187 Y- - - - -EYSVACQSDS- - - - -ACPAAEESLPLEVMVDAHKLKYENYTSFPIRDIKPPDK 239
QY 221 NITVTVARPRMLSTWQDPHSMNS- - - - -SPYRLRF- - - - -ELRYRERKKTFTYMWVKQLQNH 276
Db 240 NLOGLKL-KNSRQVSWETPDWSTPHSYFSLTFCVQVQGSKRRK- - - - -KDR- - - - - 288
QY 277 CVIHDAMSGL- - - - -RHVVQLRAQEEFGQGESEMS 307
Db 289 -VETDKTSATVICRKNASTSVRAQDRYSSSSEMA 323

RESULT 21
JQ1655
prolactin receptor precursor - chicken
C;Species: Gallus gallus (chicken)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004

C;Accession: JQ1655
R;Tanaka, M.; Maeda, K.; Okubo, T.; Nakashima, K.
Biochem. Biophys. Res. Commun. 188, 490-496, 1992
A;Title: Double antenna structure of chicken prolactin receptor deduced from the cDNA seq
A;Reference number: JQ1655; MUID:93075121; PMID:1445292
A;Accession: JQ1655
A;Molecule type: mRNA
A;Residues: 1-831 <TYN>
A;Cross-references: UNIPROT:Q04594; DDBJ:D13154; NID:g222848; P1DN:BA02439.1; P1D:g22284
A;Experimental source: kidney
C;Keywords: glycoprotein; transmembrane protein
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-831/Product: prolactin receptor #status predicted <MAT>
F;36-219/Domain: cytokine receptor homology <CRS1>
F;239-425/Domain: cytokine receptor homology <CRS2>
F;439-462/Domain: transmembrane #status predicted <TYM>
F;53,91,100,112,132,262,303,315,335,647,701,800/Binding site: carbohydrate (Asn) (covaler

Query Match 6.3%; Score 180; DB 2; Length 831;
Best Local Similarity 27.2%; Pred. No. 0.00016;
Matches 61; Conservative 31; Mismatches 96; Indels 36; Gaps 7;
QY 102 PACTVHLVDPPEPQLSCFRKPLSNVNCVEMGPRSTPLTTKAVLVRKFGNSPADP 161
Db 16 PLTTVGLAQSFPGKRIIRCRSLKERTPSCWKKFGSDGLPTNYTLF- - - - - 63
QY 162 QEPQYQSGESQK- - - - -FSCQLAVPEDSSFYI- - - - -VSMCVASVSGSKFQTKT 207
Db 64 - - - - -YSKDSSEETIECPDRTYRSGNSCYFNKNHTSPWTFENITVAINELSNSDPOY 118
QY 208 FQCGGILQDPDPANITV- - - - -TAVARNPRMLSTWQDPHSMNSFYRL-REFLRYRERSKTF 265
Db 119 VDTSTVQGVSGVNNLTLEKRSANIMYLMAKSPPLADASSNNHLYHYELRKPEKKEW 178
QY 266 TTMWVCDLQHCYIHDAMSGLAHVVQLRAQEEFGQGESEMSPE 309
Db 179 ETISV-GVQTOCKINRLNAGMYVQVRC- - - - -TLDEGESEMSSE 219

RESULT 22
150455
prolactin receptor - pigeon
C;Species: Columba livia (domestic pigeon)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: 150455
R;Chen, X.; Horeman, N.D.
Endocrinology 135, 269-276, 1994
A;Title: Cloning, expression, and mutational analysis of the pigeon prolactin receptor.
A;Reference number: 150455; MUID:94283267; PMID:7516866
A;Accession: 150455
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-830 <CHE>
A;Cross-references: UNIPROT:Q90374; EMBL:U07694; NID:g466381; P1DN:AAA20646.1; P1D:g46638
F;36-420/Domain: cytokine receptor homology <CRS1>
F;240-426/Domain: cytokine receptor homology <CRS2>
Query Match 6.2%; Score 178.5; DB 2; Length 830;
Best Local Similarity 22.0%; Pred. No. 0.0002;
Matches 90; Conservative 55; Mismatches 158; Indels 107; Gaps 19;
QY 90 DSGNSCYRAGRPACTVHLV- - - - -DVPEEPQLSCFRKPLSNVNCVEMGPRSTPLTTKA 146
Db 210 DIGEMSEMSER- - - - -HIHINPGSPPEKPTIICRSPKERTFCWKKFGSDGHPNTY 264
QY 147 VLLVRKFGNSPADPQEPQYQSGESQK- - - - -FSCQLAVPEDSSFYI- - - - -VSM 192
Db 265 TLL- - - - -YSKGEGERVYECPDYKTAGPNSCYFDKHTSFTYINITV 307
QY 193 CVASSVSGSKFQTKTQFGCGILQDPDPANITV- - - - -TAVARNPRMLSTWQDP- - - - -HSMNS 247
Db 308 KATNEIGSNVSDPLVVDVTVIQTDPVAVNILELKTIVNRKP- - - - -YLVLTWSPPLADVRSG 366

QY 248 FYRLRFLRYRAERSKTTFTTMVKDLOHHCVIHDAMSGLRHVYOLRAOEFQGESEMS 307
 A:Status: translated from GB/EMBL/DBD
 A:Molecule type: mRNA
 A:Residues: 1-917 <RE2>
 A:Cross-references: EMBL:X62646; NID:g840816; PIDN:CAA44515.1; PID:g840817

DB 367 WLTDLVLELKLKPEAEEMETIFPGQ-QTHYKMSLSPGKKYIQIHNCKPDH-HGSMSEMS 424
 C:Accession: I45971

QY 308 PE-----AMGTPWTESRS-----PPAENE-----V 327
 DB 425 LEKYLIQIPDFRIKDWVWVIVGLSSLICLVMSMTVLKGYRMAFILPPVGPRIKGI 484
 C:Accession: I45971

QY 328 STPMQALTTNNKDDNLT-----FRDSANATSLPVEFMPRPED-----SKVAAAPHQ 376
 DB 485 DTHL--LEFGKSEELLISALGCHGPPPTDCEELLITYLEVDESDQLMPSHNGHPKXN 542
 C:Accession: I45971

QY 377 PLTSSERIDKQI-RYILDGISALRKETCNKSMCESSKEA-----DAENN 420
 DB 543 AKMAIETSDSGRSGCDSPSL-SEKCRSRAILSTLQTDIRDVQENN 591
 C:Accession: I45971

RESULT 23
 145971
 prolactin receptor - bovine
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
 C:Accession: I45971
 R:Scott, P.; Kessler, M.A.; Schuler, L.A.
 Mol. Cell. Endocrinol. 89, 47-58, 1992
 A>Title: Molecular cloning of the bovine prolactin receptor and distribution of prolactin
 A:Reference number: I45971; MUID:93246019; PMID:1338725
 A:Accession: I45971
 A:Status: preliminary; translated from GB/EMBL/DBD
 A:Molecule type: mRNA
 A:Residues: 1-581 <SCO>
 A:Cross-references: UNIPROT:Q28172; GB:J02549; NID:g163617; PIDN:AAA51417.1; PID:g163618
 C:Genetic:
 A:Gene: PRLR
 F:36-221/Domain: cytokine receptor homology <CRS>

Query Match 6.0%; Score 171; DB 2; Length 581;
 Best Local Similarity 25.0%; Pred. No. 0.00041;
 Matches 51; Conservative 40; Mismatches 99; Indels 14; Gaps 7;

QY 113 PPEEPOLSCFRKSPLSNVVCEMGPSTPSLTTRAVILVRKQNSPAEDFQEPQYQSEQ 172
 DB 27 PEKPKLVKCRSPGKEFTGMEPEGADGGLPTVYTLTYHK-----EGETLHCEPDYKVTG 82
 C:Accession: A36337

QY 173 KPSQQLAVBEGDS-SFYIVSMCVASVSGSKFTQTFQCGGIIQPPRPAITVTAAARNP 231
 DB 83 PMSCYSPKHTSIWKMYVITVNAINQGISSDPLVYVTVIYVEPEPPALITLKHPEP 142
 C:Accession: A36337

QY 232 R--WLSVTQDPPSHW--SSFYRLRFLRYRAERSKTTFT--WVVKDLOHHCVIHDAMSG 286
 DB 143 RKRYLWIKSPPTMTDVKSWMFIQYIRLKPRAKADWETHFTLKQIQ--LKIENLYPQ 200
 C:Accession: A36337

RESULT 24
 149699
 glycoprotein 130 - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
 C:Accession: I49699; I48370
 R:Salto, M.; Yoshida, K.; Hibl, M.; Taga, T.; Kishimoto, T.
 J. Immunol. 148, 4066-4071, 1992
 A>Title: Molecular cloning of a murine IL-6 receptor-associated signal transducer, gp130
 A:Reference number: I48370; MUID:92291532; PMID:1602143
 A:Accession: I49699
 A:Status: translated from GB/EMBL/DBD
 A:Molecule type: mRNA
 A:Residues: 1-917 <RES>
 A:Cross-references: UNIPROT:Q00560; GB:M83336; NID:g193591; PIDN:AAA37723.1; PID:g193592
 A:Accession: I48370

A:Status: translated from GB/EMBL/DBD
 A:Molecule type: mRNA
 A:Residues: 1-917 <RE2>
 A:Cross-references: EMBL:X62646; NID:g840816; PIDN:CAA44515.1; PID:g840817

DB 118 VTMLSGFPDPKPNLTCIYNEG-KNMLCQMDGREGREYLETNTLTKSEMAETKFPD----- 171
 C:Accession: A36337

QY 161 FOEPQYQSEQKFSQQLA-VPEGDSFYI---VSMCVASVSGSKFTQTFQCGGIIQ 216
 DB 172 ----CQSKHGT---SCWVSYP---TYVYVIEVWVEALNALGVSESIINFDPVDKVP 220
 C:Accession: A36337

Query Match 5.9%; Score 167.5; DB 2; Length 917;
 Best Local Similarity 25.0%; Pred. No. 0.0013;
 Matches 58; Conservative 48; Mismatches 89; Indels 37; Gaps 12;

QY 106 VHLVVDVPEEP-QSCFRKSPLSNVVCEMGP-RST---PSLTTRAVILVRKQNSPAED 160
 DB 118 VTMLSGFPDPKPNLTCIYNEG-KNMLCQMDGREGREYLETNTLTKSEMAETKFPD----- 171
 C:Accession: A36337

QY 217 DPPANITVTAARNPMLSVTQDPPSHWSSFYRLRFLRYRAERSKTTFTTMVKDLOH- 275
 DB 221 TRPYMLSVTNSELSILKLSWVS--SGGGLDLKSDIQY--RTKQASTWLVQVLEDT 275
 C:Accession: A36337

QY 276 -----HCVIHDAMSGLRHVYOLRAOEFQGESEMSPPAMGTPWTESRSP 322
 DB 276 MSRTSFTVQDLKPFTEYVFRIRISDKSGKGYMSDSEASGTTTYEDRSRP 327
 C:Accession: A36337

RESULT 25
 A36337
 membrane glycoprotein gp130 precursor - human
 C:Species: Homo sapiens (man)
 C:Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 09-Jul-2004
 C:Accession: A36337
 R:Hibl, M.; Murakami, M.; Salto, M.; Hirano, T.; Taga, T.; Kishimoto, T.
 Cell 63, 1149-1157, 1990
 A>Title: Molecular cloning and expression of an IL-6 signal transducer, gp130.
 A:Reference number: A36337; MUID:91084844; PMID:2261637
 A:Accession: A36337
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-918 <HIB>
 A:Cross-references: UNIPROT:P40189; GB:M57230; NID:g186353; PIDN:AAA59155.1; PID:g186354
 C:Genetic:
 A:Gene: GDB:IL6ST; GP130
 A:Cross-references: GDB:126725; OMIM:600694
 A:Map position: 5q11-5q11
 C:Keywords: glycoprotein; membrane protein
 F:334-316/Domain: cytokine receptor homology <CRS>

Query Match 5.9%; Score 167.5; DB 2; Length 918;
 Best Local Similarity 22.1%; Pred. No. 0.0013;
 Matches 82; Conservative 61; Mismatches 133; Indels 95; Gaps 19;

QY 106 VHLVVDVPEEP-QSCFRKSPLSNVVCEM-GPRST---PSLTTRAVILVRKQNSPAED 160
 DB 118 ITISGLPPEKPNLTCIYNEG-KKRCCEMDGREGREYLETNTLTKSEMAETKFPD----- 171
 C:Accession: A36337

QY 161 FOEPQYQSEQKFSQQLAVBEGDSFYIVSMCV---ASSVSGSKFTQTFQCGGIIQ 216
 DB 172 ----CKAKDTPR-CTVYV---STVYVYVIEVWVEALNALGVSHINFPVYKVP 222
 C:Accession: A36337

QY 217 DPPANITVTAARNPMLSVTQDPPSHWSSFYRLRFLRYRAERSKTTFTTMVKDLOH--L 273
 DB 223 NPHNLSVINSELSILKLTWNPIS--KSVIILKYNQYRKQASTWSQIAPREDTAST 280
 C:Accession: A36337

QY 274 QHHCVIHDAMSGLRHVYOLRAOEFQGESEMSPPAMGTPWTE--SRSP-----PAE 324
 DB 281 RSFTVQDLKPFTEYVFRIRCKEDGKGYMSDSEASGITTYEDRPSKAPSFYKIDPSH 340
 C:Accession: A36337

QY 325 NE-----VSTPMQ-----LTTNKDD----- 341
 C:Accession: A36337

Db 341 TCGRTVQLVWKTLPPEFANGKILDYEVLTTRKSHLQNYVYATATGLTINLNDRYLATL 400
 Qy 342 ---NIFRISANTSLPV-EFMVPPGEGSKDVAAPHROP-----TSSERIDKQIRYL 392
 Db 401 TVRNVLGSKDDAVLTTPACDFQATHFVMDLK--APFKDMLVWETTPRESVYK---YIL 455
 Qy 393 DGISALRKETC 403
 Db 456 EWCVLSDKAPC 466

RESULT 26

A44257
 Interleukin-6 signal transducing molecule gp130 - rat
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
 C/Accession: A44257
 R/Wang, Y.; Neelbitt, J.E.; Fuentes, N.L.; Fuller, G.M.
 Genomics 14, 666-672, 1992
 A/Title: Molecular cloning and characterization of the rat liver IL-6 signal transducing
 A/Reference number: A44257; MUID:93052397; PMID:1427893
 A/Status: preliminary; not compared with conceptual translation
 A/Molecule type: mRNA
 A/Residues: 1-918 <MAN>
 A/Cross-references: UNIPROT:P40190
 A/Experimental source: liver
 A/Note: sequence extracted from NCBI backbone (NCBI:P118488)
 C/Keywords: transmembrane protein
 F,134-315/Domain: cytokine receptor homology <CRS>

Query Match 5.8%; Score 166; DB 2; Length 918;
 Best Local Similarity 20.2%; Pred. No. 0.0017;
 Matches 99; Conservative 71; Mismatches 171; Indels 150; Gaps 22;
 Qy 106 VHLIVDVPPEP-QLSCFRKSPLSNVCEWGP-RST---PSLTKAVLVRKFGNSAED 160
 Db 118 ITILSGVPDIPMLSLCIVNEG-KQMLCQDPRGRETLETNYTLKSSWATEKEPD----- 171
 Qy 161 FQEPQYQSOSQKFSQCLAVEGDSFYIVSMCV---ASSVGSKFSKTQTFQGCGLIOP 216
 Db 172 ---CRTRKHTGS--SCMM---GYTPYFVNIWVEAENALGNVSEPIINFDPVDKVP 221
 Qy 217 DDPANITVTVAARNPMLSTWQDPHSMNSFTRLRFLARBRSKTFTTMVKLOH- 275
 Db 222 SPFNLSVTNSELSTILKLA--VNSGLDSILRLKSDIQY---RTKDASTWIOVLEDT 276
 Qy 276 ---HCVIDHANSGLRHVVOLRAQEFQGESEMSPEAMGTPTMTE--SRSP----- 321
 Db 277 VSPRTSFTVODLKPFEYVFRIRSIKENGKGYWSDMSEASGTTIEDRPSKAFSFWYKN 336
 Qy 322 ---PAE-----NEVSTPMQALTTNKD----- 340
 Db 337 ANHFOETRSARLWKTLPLSEANGKILDYEVLTQSKSVQTYVANGTELIIVLTNNRYV 396
 Qy 341 ---DNILFRDSANATSLP-VFMPVPVPGEDSKDVA-----APHRQPLTSEKRD 385
 Db 397 ASLAARVVGKSPATVLTITGSHFKASHRPVVDLKAPPKDNLWVETTPPSKPVN----- 450
 Qy 386 KQRIYILIDGISARKETCNKSNMCESSKEALAEENLIPMAEKQCFQSGFNEETCLVK 445
 Db 451 ---KYL-----EWG-----VLSNSPCIDMQOEDGTVAR-----TH 480
 Qy 446 IITGLFEFYLYEYLQNRFSSEQARAVQMTKULIQLOKKAKKULDIATTPDPTNAS 505
 Db 481 LRSSLLESKCYLITVPVFPFGGSGPESM-----KAYLKQAAPSKGPTVART 527
 Qy 506 LLTUKLOAQNQW 516
 Db 528 KYGKNEAVLEW 538

RESULT 27

A30304
 prolactin receptor 2 precursor - rabbit
 N/Alternate names: prolactin receptor, mammary gland
 C/Species: Oryctolagus cuniculus (domestic rabbit)
 C/Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
 C/Accession: A30304; A60380
 R/Edey, M.; Jolicoeur, C.; Levi-Meynueis, C.; Duaner-Fourt, I.; Petridou, B.; Boutin,
 Proc. Natl. Acad. Sci. U.S.A. 86, 2112-2116, 1989
 A/Title: Identification and sequence analysis of a second form of prolactin receptor by n
 A/Reference number: A30304; MUID:89184578; PMID:2288321
 A/Accession: A30304
 A/Molecule type: mRNA
 A/Residues: 1-616 <EDE>
 A/Cross-references: UNIPROT:P14787; GB:J04510; NID:G165669; PIDN:AAA31457.1; PID:G165670
 R/Waters, M.J.; Spencer, S.A.; Hamlin, G.; Henzel, W.J.; Wood, W.I.
 Int. J. Biochem. 22, 1089-1095, 1990
 A/Title: Purification and partial sequence of the rabbit mammary gland prolactin receptor
 A/Reference number: A60380; MUID:91146782; PMID:2289615
 A/Accession: A60380
 A/Molecule type: protein
 A/Residues: 41-58, 'X', 60-66; 90-93, 'X', 95-96, 'X', 98-103, 'X', 105, 'NX', 108, 150-164, 'XX', 167-
 A/Note: the amino end of the mature protein was blocked
 C/Keywords: blocked amino end; glycoprotein; transmembrane protein
 F,1-24/Domain: signal sequence #status predicted <SIG>
 F,25-616/Product: prolactin receptor 2 #status predicted <MAT>
 F,36-221/Domain: cytokine receptor homology <CRS>
 F,225-258/Domain: transmembrane #status predicted <TM>
 F,59,104,132,347,389,411/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 5.6%; Score 161.5; DB 2; Length 616;
 Best Local Similarity 21.8%; Pred. No. 0.002;
 Matches 71; Conservative 42; Mismatches 141; Indels 71; Gaps 11;
 Qy 113 PPEEPQLSCFRKSPLSNVCEWGPSPSTSLTKAVLTVLRKTONSPAEDFQEPQYQSQ 172
 Db 27 PGKPFIFKCRSPERKEFTLCWWRPGADGLPTNVTLYTHK-----EGRTTTECDYKTKG 82
 Qy 173 KFSQCLAVEBGDS-SFYVSMCAVSSVGSKFSKTQTFQGCGLIOPDPANITVTVAARNP 231
 Db 83 PMSCTFSKSHGISMTYITITVATNQGSVSDRYVDVTYIVBDDPVNLTLEVKHPED 142
 Qy 232 R--WLSVTWDPH--SNNSSFYRLRFLRYARERSKFTTMMVKLOLHNCYIHDAMGSLR 287
 Db 143 RKPVLWVWMLPPTLVDVNSGULTIOYELRLKPEKAEMHTHPAQ-QTFKILSLVYQCK 201
 Qy 268 HVOURLAEERFGQEGMSWSPRA-----M 311
 Db 202 YLVQVRCKPD--HGFWSVSPSSSIQIPNDFTMKDITWIFVAVLTICLIWMAVALK 259
 Qy 312 GTPWTERSPPAENEVSTP-----MQALTTNKDDNIL-----FRDSANATSLPVEFM 359
 Db 260 GYSWVTCIFPP-----VGPRIKGFDTLLEKGSBELLSAFGCODFPPTACEDLVEFL 315
 Qy 360 PVPFGED-----SKDVAAPHROP 377
 Db 316 EVDSSEDOQLMPAHSKHSFGMKP 340

RESULT 28

A29884
 prolactin receptor precursor - rat
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004
 C/Accession: A29884
 R/Boutin, J.M.; Jolicoeur, C.; Okamura, H.; Gagnon, J.; Edey, M.; Shirota, M.; Banville,
 Cell 53, 69-77, 1988
 A/Title: Cloning and expression of the rat prolactin receptor, a member of the growth hor
 A/Reference number: A29884; MUID:8815059; PMID:2832068
 A/Accession: A29884
 A/Molecule type: mRNA
 A/Residues: 1-310 <BOU>
 A/Cross-references: UNIPROT:P05710; GB:J019304; NID:G206364; PIDN:AAA41937.1; PID:G206365

A>Title: Expression of multiple forms of the prolactin receptor in mouse liver.
 A/Reference number: 157699; NID:89261824; PMID:2725531
 A/Accession: 177524
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-303 <RES>
 A/Cross-references: UNIPROT:Q08501; GB:M22958; NID:g200479; PIDN:AAA39976.1; PID:g200480
 F:31-216/Domain: cytokine receptor homology <CRS>

Query Match 5.4%; Score 155; DB 2; Length 303;
 Best Local Similarity 22.6%; Pred. No. 0.0022;
 Matches 49; Conservative 35; Mismatches 91; Indels 42; Gaps 8;

113 PREEPOLSCFRKSPLENNVCEWGPSTPSLTAKAVLLVRKFGNSPAEDPEPCQYQSEQ 172
 DB PPKPEIHKCRSPDKETFTCMWNPSSDGLPTNYSL-----TYSKEGE 64

QY 173 K--FSCQLAVPEGDSS-----FYISMCAVSSVGSFKSKTQTFQGGIQLQDP 218
 DB KMTYECPDYKTSQPNSCFSPSKOYTSIMKIYIITVNAITNMGSSSTSDPLVYDVYIYEPER 124

QY 219 PANIT--VTAVANRPMLSVTWDP--HSWNSFYLRLRYRARSKTFTTWVVKDQ 274
 DB PNLTLEVLQKDKKTYLWVKMLPPTITDVKTGMFTMEYEIRLKSSEA---DEMEIHFTG 181

QY 275 HHC--VIHDAMSGLRHVQLRAQEEFGQGESEMSPE 309
 DB HQTQFKVFDLYPGQKYLVTQCKPD--HGWSRMQGE 216

RESULT 36
 153269
 prolactin receptor, long form - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 02-Aug-1996 #sequence revision 02-Aug-1996 #ext_change 09-Jul-2004
 C/Accession: 153269; J06671; S34356
 R:Clarke, D.L.; Linzer, D.I.H.
 Endocrinology 133, 224-232, 1993
 A>Title: Changes in prolactin receptor expression during pregnancy in the mouse ovary.
 A/Reference number: 153269; NID:93307149; PMID:8319571
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-608 <RES>
 A/Cross-references: UNIPROT:Q08501; GB:L14811; NID:g293769; PIDN:AAA02686.1; PID:g293770
 R:Moore, R.C.; Oka, T.
 Gene 134, 263-265, 1993
 A>Title: Cloning and sequencing of the cDNA encoding the murine mammary gland long-form
 A/Reference number: J06671; NID:94085788; PMID:8262385
 A/Accession: J06671
 A/Molecule type: mRNA
 A/Residues: 1-608 <MOO>
 A/Cross-references: GB:L13593; NID:g347398; PIDN:AAC37641.1; PID:g347842
 R:Edery, M.; Pezet, A.; Nandi, S.; Kelly, P.A.
 submitted to the EMBL Data Library, June 1993
 A/Description: Isolation and nucleotide sequence of a mouse cDNA prolactin receptor.
 A/Reference number: S34356
 A/Accession: S34356
 A/Molecule type: mRNA
 A/Residues: 1-557, 'F', 559-608 <EDE>
 A/Cross-references: EMBL:X73372; NID:g312696; PIDN:CAA51789.1; PID:g312697
 C/Comment: Prolactin receptor have long form and short form which are resulted from alternative splicing. This long form receptor is capable of transducing a signal to milk protein gene
 C/Keywords: receptor; transmembrane protein
 F:31-216/Domain: cytokine receptor homology <CRS>
 F:230-253/Domain: transmembrane #status predicted <TM>

Query Match 5.4%; Score 155; DB 2; Length 608;
 Best Local Similarity 22.6%; Pred. No. 0.0056;
 Matches 49; Conservative 35; Mismatches 91; Indels 42; Gaps 8;

QY 113 PREEPOLSCFRKSPLENNVCEWGPSTPSLTAKAVLLVRKFGNSPAEDPEPCQYQSEQ 172
 DB PPKPEIHKCRSPDKETFTCMWNPSSDGLPTNYSL-----TYSKEGE 64

DB 22 PPKPEIHKCRSPDKETFTCMWNPSSDGLPTNYSL-----TYSKEGE 64

QY 173 K--FSCQLAVPEGDSS-----FYISMCAVSSVGSFKSKTQTFQGGIQLQDP 218
 DB KMTYECPDYKTSQPNSCFSPSKOYTSIMKIYIITVNAITNMGSSSTSDPLVYDVYIYEPER 124

QY 219 PANIT--VTAVANRPMLSVTWDP--HSWNSFYLRLRYRARSKTFTTWVVKDQ 274
 DB PNLTLEVLQKDKKTYLWVKMLPPTITDVKTGMFTMEYEIRLKSSEA---DEMEIHFTG 181

QY 275 HHC--VIHDAMSGLRHVQLRAQEEFGQGESEMSPE 309
 DB HQTQFKVFDLYPGQKYLVTQCKPD--HGWSRMQGE 216

RESULT 37
 A53743
 protein-tyrosine kinase (BC 2.7.1.112) tyrosine precursor - human
 N/Alternate names: protein-tyrosine kinase sky; receptor-type tyrosine kinase rse
 C/Species: Homo sapiens (man)
 C/Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #ext_change 09-Jul-2004
 C/Accession: A53743; J00077; J02145; S32765; S32219
 R:Marx, M.R.; Scadden, D.T.; Wang, Z.; Gu, Q.; Goddard, A.; Godowski, P.J.
 J. Biol. Chem. 269, 10720-10728, 1994
 A>Title: rse, a novel receptor-type tyrosine kinase with homology to Axl/Ufo, is expressed
 A/Reference number: A53743; NID:94193774; PMID:7511603
 A/Accession: A53743
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-890 <MAR>
 A/Cross-references: UNIPROT:Q06418; GB:U05682; NID:g463469; PIDN:AAA19236.1; PID:g463470
 R:Ohnishi, K.; Mizuno, K.; Kume, K.; Miyata, T.; Nakamura, T.
 Oncogene 9, 699-705, 1994
 A>Title: Cloning of the cDNA for a novel receptor tyrosine kinase, Sky, predominantly expressed
 A/Reference number: J00077; NID:94150991; PMID:8108112
 A/Accession: J00077
 A/Molecule type: mRNA
 A/Residues: 1-890 <OHA>
 A/Cross-references: DBJ:DJ7517; NID:g624880; PIDN:BAA04467.1; PID:g624881
 A/Experimental source: hepatoma HepG2 cell
 R:Polvi, A.; Armstrong, E.; Lai, C.; Lemke, G.; Huebner, K.; Spritz, R.A.; Guida, L.C.; R
 Gene 134, 289-293, 1993
 A>Title: The human TYRO3 gene and pseudogene are located in chromosome 15q14-q25.
 A/Reference number: J02145; NID:94085793; PMID:8262388
 A/Accession: J02145
 A/Molecule type: mRNA
 A/Residues: 519-790 <POL>
 A/Cross-references: EMBL:X72886; NID:g296020; PIDN:CAA51396.1; PID:g312336
 R:Polvi, A.; Armstrong, E.; Lai, C.; Lemke, G.; Huebner, K.; Aitalo, K.
 submitted to the EMBL Data Library, March 1993
 A/Description: Human TYRO3 gene and pseudogene in chromosome 15pter-q25.
 A/Reference number: S32219
 A/Accession: S32219
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 519-790 <PO2>
 A/Cross-references: EMBL:X72886; NID:g296020; PIDN:CAA51396.1; PID:g312336
 C/Genetics:
 A/Genes: GDB:TYRO3
 A/Cross-references: GDB:134764; OMIM:600341
 A/Map position: 15q15.1-15q21.1
 C/Superfamily: protein-tyrosine kinase axl; fibronectin type III repeat homology; immunoglobulin
 C/Keywords: ATP; brain; glycoprotein; growth factor receptor; phosphotransferase; transmembrane
 F:1-41/Domain: (or 7-41) signal sequence #status predicted <Sig>
 F:42-890/Product: protein-tyrosine kinase tyrosine #status predicted <MAT>
 F:60-119/Domain: immunoglobulin homology <IMM1>
 F:156-205/Domain: immunoglobulin homology <IMM2>
 F:224-309/Domain: fibronectin type III repeat homology <FN3A>
 F:322-405/Domain: fibronectin type III repeat homology <FN3B>
 F:429-451/Domain: transmembrane #status predicted <TM>
 F:516-793/Domain: protein kinase homology <KIN>
 F:524-532/Region: protein kinase ATP-binding motif
 F:63,191,230,240,293,366,380/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 5.1%; Score 146; DB 1; Length 890;
 Best Local Similarity 23.1%; Pred. No. 0.039; Indels 128; Gaps 18;
 Matches 83; Conservative 30; Mismatches 119;

9 LALLAAGAAALAPRCPOAEVARGV---LTSIPGDSVLTTCGVEPEEDNATVHV--- 61
 23 LGLLALASLILPESAAAGLKLMGAPVULTVSQGPVTLNC-SVEGMSEPDIOGWKGA 81
 62 -----LRRPAGSHPSRMAWGMGRLLRSVOLHDSGNYSCY-----RAGRPA----- 103
 82 VVQNLDTLYIPVSEQH---WIGF---LSLKSVERSDAGRYWCQVEDGETEISQPVWLT 135
 104 -GYVHLLVD-----VPREP-QLSCFKPSPLSNVVCW-----GPRSTPSLTTKAVL 148
 136 EGVPTFVEPRDLAVPNAAPQLSCENAVGPEPVITVWMTGKIGGAPAPSPVAVTGV 195
 149 LVKRFQNSPADPQEPQYQSQFSQQLAVPEBDSFFIVSMCVASVSGSKFTQTF 208
 196 -----TQSTMFSCAHNLKGLAS-----SRTATV 219
 209 GCGGILQ--DPPRNTTNTVANRPRMLSVTV-----QDPHSMNSSE 248
 220 H-----LQALPAPAFITVTKLSSN--ASVAMMGADGRALLQSCITVQVQAFQGW---- 269
 249 YRLRFELRYRARSKTFTTMMVKDLQHNCHVIDAMSGLRHVQVLRQAEFGQGEWSEMP 308
 270 -----EVLAVVVPVPPFT-----CLLRDVLVPATNTSLRVCANALGPSPYADWVP 314

RESULT 38

Down syndrome cell adhesion protein 1 - human (fragment)
 N:Alternate names: Down syndrome cell adhesion molecule
 C:Species: Homo sapiens (man)
 C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 11-Jun-1999
 C:Accession: T08851
 R:Yamakawa, K.; Huo, Y. K.; Haendel, M. A.; Hubert, R.; Chen, X. N.; Lyons, G. E.; Korenberg
 submitted to the EMBL Data Library, September 1997
 A:Description: DSCAM: A novel member of the immunoglobulin superfamily maps in a down sy
 A:Reference number: Z16495
 A:Accession: T08851
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1896 <YAM>
 A:Cross-references: EMBL:AF023449; NID:G3169765; PID:G3169766
 A:Experimental source: brain; developmental stage: 14 weeks; fetal
 C:Genetics:
 A:Gene: DSCAM
 A:Map position: 21q22
 A>Note: derived from alternately-spliced mRNA
 C:Function:
 A:Description: involved in nervous system development
 C:Keywords: alternative splicing

Query Match 5.0%; Score 144; DB 2; Length 1896;
 Best Local Similarity 23.8%; Pred. No. 0.15; Indels 153; Gaps 15;
 Matches 81; Conservative 49; Mismatches 153;

24 RCPAQEVN-RGVLTSLPQDSVTLTCGVEPEEDNATVHWLRKPAAGSHPSRMAGMGR-- 80
 1269 KAPARILTFSGTVTTPMKKIDILPCKAV-GDPSPAVPM--KDSNGT-PSLVITIDGRKSI 1324
 81 -----LLRSVOLHDSGNYSCY---RAGRPAGYVHLLVNDVPEPRQLSCFRKPSPLSNVC 132
 1325 FSNQSFITRTVKAEDSGYISCLANNMGSDIILNLQVQVPPDQPRILT-VSKTSSSITL 1383
 133 EMGPRSTPSLTTKAVLVKRFQV-----SPAEDPQECQYQSQFSQQLA 179
 1384 SWLPDNGSGSIRGYILQYSEBNSQWSPFIPSEK-----SYRLNKLKGTWYKFTLT 1438
 180 VREGSSPFIVSMCVASVSGS--KFSKQTFQCGGILQDPDPANITVTAVANRPRMLSVT 237

Db 1439 AONGVGRGISLIEAKTLGKEPQFSKEQELF-----ASINTTRVLN-----LIG 1484

Qy 238 WDPHSMNSSPFRLRRELATYRARSKTFTTMMVKDLQHNCHVIDAMSGLRHVQVLRQAE 297
 Db 1485 WNDGCGPITS-----FTLLYRPRGTTVWTTAORTSLSKSYILYDQBATWELQWRVNS 1539

Qy 298 FQGEWSEMPPEAMGTPTWTESSRPPAENEVSTPMQALTNK 338
 Db 1540 AG---CAEKQANFATLNTYGSTIPPLIKSVQNEBGLTNE 1577

RESULT 39

prolactin receptor short form S1b precursor, breast cancer cells T-47D - human
 C:Species: Homo sapiens (man)
 C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
 C:Accession: B59405; B49400
 R:Hu, Z. Z.; Meng, J.; Dufau, M. L.
 J. Biol. Chem. 276, 41086-41094, 2001
 A:Title: Isolation and characterization of two novel forms of the human prolactin recept
 A:Reference number: A59405; MUID:21538812; PMID:11518703
 A:Accession: B59405
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-288 <HU1>
 A:Cross-references: UNIPROT:Q96P36; GB:AF214012; PIDN:AF214012.1
 R:Hu, Z. Z.
 submitted to GenBank, December, 1999
 A:Reference number: A49400
 A:Accession: B49400
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-288 <HU2>
 A:Cross-references: GB:AF214012; PIDN:AF214012.1
 A:Comment: This is one of the short forms (S1a and S1b) of the human prolactin receptor g
 ta-casain gene promoter activation, with S1b more effective than S1a. However, their lig
 C:Genetics:
 A:Gene: GDB:PRLR
 A:Cross-references: GDB:120315; OMIM:176761
 A:Map position: 5p13.3-5p13.1
 C:Keywords: glycoprotein; transmembrane protein
 F:1-24/Domain: signal sequence #status predicted <SIG>
 F:25-288/Product: prolactin receptor, short form S1b #status predicted <MAT>
 F:36-221/Domain: cytokine receptor homology <CRS>
 F:59,104,233/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 4.8%; Score 138; DB 2; Length 288;
 Best Local Similarity 22.1%; Pred. No. 0.031; Indels 52; Gaps 8;
 Matches 49; Conservative 32; Mismatches 89;

Qy 112 VPPEPQLSCFRKPSPLSNVVCWGPSTPSLTTKAVLVKRFQNSPADPQEPQYQSQDS 171
 26 LPFGKPEIFKCRSPNKETFTCMWRPGLDGLPTNYSLTVHR-----EGET 70
 172 QKFSQQLAVPEBDS-----FYVSMCVASVSGSKRKTQFGCGILOPDP 219
 Db 71 LMRHCPRYITGGPNSCHFGKQYTSMMRTYIMVATNQGSSFSDELVDYVITVQPP 130
 220 ANITVTAVANRPR--WISVTWQDPH--SWNSFYRLRFELRYRARSKTFTTMMV----- 270
 Qy 131 LELAVEYKQPRDRKPYLMIKSPPTLIDKTGMFTLLYELRLPEKA---AEWEIHFAQ 187
 271 -----KDLOHCHVIDAMSGLRHVQVLRQAEFGQGEWSEMP 308
 Db 188 QTEFKILSLH-----FGQKYLVOVRCKPD--HGYSAMSP 220

RESULT 40

prolactin receptor short form S1a precursor, breast cancer cells T-47D - human
 C:Species: Homo sapiens (man)
 C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
 C:Accession: A59405; A49400

R;Hu, Z.Z.; Meng, J.; Dufau, M.L.

J. Biol. Chem. 276, 41086-41094, 2001

A/Title: Isolation and characterization of two novel forms of the human prolactin receptor

A;Reference number: A59405; MUID:21538812; PMID:115187033
A;Title: Isolation and characterization of two novel *IoT*

A;Reference number: A59405

A;Accession: A59405
A;Status: preliminary

A;Status: preliminary
A:Molecule type: DNA

A;Molecule type: DNA

A;Residues: 1-376 <HU1>

A;Cross-references: UNIPROT:Q96P35;

R;Hu, Z.Z.

submitted to GenBank, December, 1999

A:Reference number: A49400

A;Reference number: A49400
A;Accession: A49400

A;Accession: A49400

A;Status: preliminary

A;Molecule type: DNA

```

n/nucleotide 2760: DNA
A;Residues: 1-376 <HU2>

```

A;Cross-references: GB:AF214012; PIDN:AF214012.1

C;Comment: This is one of the short forms (S1a and S1b) of the human prolactin receptor

c;Comment: This is one of the short forms (S1a and S1b) of the human prolactin receptor gene promoter activation, with S1a being effective than S1b. However, their

eta-cashejn gene
fed COS-1 and HE

ted COS-1 and HEK293 cells is due to rapid

C;Genetics:

A;Gene: GDB:PRLR

A;Cross-references: GDB:120315; OMIM:176761

A;CIBBS-References: GDB:120313; OMIM:116761
A;Map position: 5p13.3-5p13.1

A:map position: 5pL3.3-5pL3.1
C:Keywords: glycoprotein; transmembrane protein

C;Keywords: glycoprotein; transmembrane protein
E:1-24/Domain: signal sequence #status predicted <STG>

F;1-24/Domain: signal sequence #status predicted <SIG>
E;35-376/Product: projection receptor short form S1a #status pre

F;25-376/Product: prolactin receptor, short form Sla #status pre

F:36-221/Domain: cytokine receptor homology <CRS>

F;59,104,233/Binding site: carbohydrate (Abn) (covalent) #status predicted

DATE: 06/09/2007
TIME: 10:07 AM
PAGE: 1

Query Match 4.8%; Score 138; DB 2; Length 376;

Query Match	4.88;	Score 138;	DB 2;	Length 3/6;
Best Local Similarity	22.18;	Pred. No. 0.044;		

Best Local Similarity 22.1%; Pred. No. 0.044;
Matches 49: Conservative 32: Mismatches 89: Indels 52: Gaps 8

Matches 49; Conservative 32; Mismatches 89; Indels 52; Gaps 8

1.1.3 **WENNBEZUGSVERHÄLTNISSE**

112 VPPEEPQLSCFRKSPLSNVCEWGPSTPSTTKAVLLVRKFQNSPAEDFQEPQYSQES 171

[illegible]

Db 26 LPPGKPEIFKCRSPNKETFTCWRPPTDGLPTNYSLYHR-----EGET 70

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 9, 2004, 08:40:41 ; Search time 249.038 Seconds
(without alignments)
1254.542 Million cell updates/sec

Title: US-09-462-416-7

Perfect score: 2861

Sequence: 1 MNAVGCALLALALAPGAL.....LILRSFKETLQSLRALRQM 543

Scoring cable: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1918	67.0	468	1	IL6A_HUMAN
2	1468	51.3	467	1	IL6A_PIG
3	991	34.6	462	1	IL6A_RAT
4	954.5	33.4	460	1	IL6A_MOUSE
5	938.5	32.8	212	1	IL6_HUMAN
6	938.5	32.8	212	2	AA807539
7	938.5	32.8	212	2	CAG29292
8	907.5	31.7	212	1	IL6_MACFA
9	899.5	31.4	212	1	IL6_MACMU
10	898.5	31.4	209	2	O97540
11	895.5	31.3	212	1	IL6_CERTR
12	801.5	28.0	212	2	O8MKH0
13	799.5	27.9	209	2	O9THH3
14	617.5	21.6	175	2	O9THH4
15	577	20.2	207	2	O9MYZ7
16	574.5	20.1	209	1	IL6_PHOVI
17	571.5	20.0	208	1	IL6_HORSE
18	571	20.0	205	1	IL6_ORCOR
19	562	19.6	208	2	O9XT80
20	561	19.6	207	1	IL6_CANPA
21	558	19.5	211	1	IL6_LAMGL
22	558	19.5	211	2	O865W7
23	557.5	19.5	212	1	IL6_PIG
24	555.5	19.4	212	2	O8MJ75
25	544.5	19.0	208	1	IL6_FELCA
26	539.5	18.9	160	2	O97535
27	516.5	18.1	207	2	O28403
28	501.5	17.5	214	2	O8MKES
29	482.5	16.9	191	2	O6QHY3
30	482.5	16.9	191	2	AA873282
31	472	16.5	208	1	IL6_CAPRI

32	471	16.5	208	1	IL6_BOVIN	P26892 bos taurus
33	467	16.3	208	1	IL6_SHEEP	P29455 ovine aries
34	466	16.3	208	2	O6V919	O6V919 bubalus bub
35	466	16.3	208	2	AA054301	AA054301 bubalus b
36	437.5	15.3	207	1	IL6_MARMO	O35736 marmota mon
37	435.5	15.2	207	2	O9JHH3	O9JHH3 marmota mon
38	403.5	14.1	528	2	O6UANS	O6UANS tetraodon n
39	403.5	14.1	528	2	AA825684	AA825684 tetraodon n
40	396.5	13.9	211	1	IL6_RAT	P20607 rattus norv
41	382	13.4	241	2	O9MZRI	O9MZRI oryctolagus
42	378	13.2	212	2	O91ZL3	O91ZL3 sigmodon hl
43	374.5	13.1	211	1	IL6_MOUSE	P08505 mus musculu
44	371	13.0	210	2	O9WV08	O9WV08 mesocricetu
45	355	12.4	241	2	O90Y10	O90Y10 gallus gall

ALIGNMENTS

RESULT 1	IL6A_HUMAN	STANDARD;	PRT;	468 AA.
ID	IL6A_HUMAN			
AC	P08887; Q16202;			
DT	01-NOV-1988 (Rel. 09, Created)			
DT	01-NOV-1988 (Rel. 09, Last sequence update)			
DT	01-OCT-2004 (Rel. 45, Last annotation update)			
DE	Interleukin-6 receptor alpha chain precursor (IL-6R-alpha) (IL-6R 1)			
DE	(CD126 antigen).			
GN	Name=IL6R;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RX	MEDLINE=8305347; PubMed=316546;			
RA	Yamaoka K., Taga T., Hirata Y., Yawata H., Kawanishi Y., Seed B.,			
RA	Taniguchi T., Hirano T., Kishimoto T.;			
RT	Molecular structure of interleukin 6 receptor."			
RL	Proc. Jpn. Acad. B, Phys. Biol. Sci. 64:209-211(1988).			
RN	[3]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RX	MEDLINE=91336983; PubMed=1872801;			
RA	Schooltink H., Stoyan T., Lenz D., Schmitz H., Hirano T.,			
RA	Kishimoto T., Heinrich P.C., Rose-John S.;			
RT	"Structural and functional studies on the human hepatic interleukin-6			
RL	receptor. Molecular cloning and overexpression in HepG2 cells."			
RL	Biochem. J. 277:659-664(1991).			
RN	[4]			
RP	SEQUENCE OF 313-365 FROM N.A. (ISOFORM 2).			
RX	MEDLINE=94333499; PubMed=8056053;			
RA	Horiuchi S., Koyanagi Y., Zhou Y., Miyamoto H., Tanaka Y., Waki M.,			
RA	Matsumoto A., Yamamoto M., Yamamoto N.;			
RT	"Soluble interleukin-6 receptors released from T cell or			
RT	granulocyte/macrophage cell lines and human peripheral blood			
RT	mononuclear cells are generated through an alternative splicing			
RT	mechanism."			
RL	Eur. J. Immunol. 24:1945-1948(1994).			
RN	[5]			
RP	PARTIAL SEQUENCE, CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.			
RX	MEDLINE=99167486; PubMed=10066782;			
RA	Cole A.R., Hall N.E., Treutlein H.R., Eddes J.S., Reid G.E.,			
RA	Moritz R.L., Simpson R.V.;			
RT	"Disulfide bond structure and N-glycosylation sites of the			
RT	extracellular domain of the human interleukin-6 receptor."			
RL	J. Biol. Chem. 274:7207-7215(1999).			


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FT STRAND 34 37
TT TURN 39 40

Query Match 67.0%; Score 1918; DB 1; Length 468;
Best Local Similarity 96.5%; Pred. No. 1,1e-126;
Matches 360; Conservative 1; Mismatches 4; Indels 8; Gaps 1;

QY 1 MLAVGALLAALAAFGAALAPRCPAEOVARGVLTSLPDGSLTLTCGVEPNDNTVM 60
DB 1 MLAVGALLAALAAFGAALAPRCPAEOVARGVLTSLPDGSLTLTCGVEPNDNTVM 60
QY 61 VLKRPAGSHPSWAGMGRRLILRSVQLHDSGNYSCYRAGRPAQVHLVDPVEEPOLS 120
DB 61 VLKRPAGSHPSWAGMGRRLILRSVQLHDSGNYSCYRAGRPAQVHLVDPVEEPOLS 120
QY 121 CFRKSPLSNVVCGWGRSTPSLTTKAVLVKRFQNSPAEDFOBPCCOYSQSFSCQLAV 180
DB 121 CFRKSPLSNVVCGWGRSTPSLTTKAVLVKRFQNSPAEDFOBPCCOYSQSFSCQLAV 180
QY 181 PEGDSSFYIVSMCVASSVSGSKFQTFQCGILQDPDPANITVTVANRPRMLSTWOD 240
DB 181 PEGDSSFYIVSMCVASSVSGSKFQTFQCGILQDPDPANITVTVANRPRMLSTWOD 240
QY 241 PHSWNSFYRLRPELRYRERSKFTTMMVKDQHCVIDHWSGLRHVVQLRAQEFQ 300
DB 241 PHSWNSFYRLRPELRYRERSKFTTMMVKDQHCVIDHWSGLRHVVQLRAQEFQ 300
QY 301 GEMSESPKAMGTPWTESSPPAENEVSTPMQALTNKDDNILFRDSANATSLPYEFMP 360
DB 301 GEMSESPKAMGTPWTESSPPAENEVSTPMQALTNKDDNILFRDSANATSLPYEFMP 360
QY 361 VPRGDSKDVAP 373
DB 357 ----QDSSVPLP 365

RESULT 2
IL6A_PIG STANDARD; PRT; 467 AA.
AC 018766;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interleukin-6 receptor alpha chain precursor (IL-6R-alpha) (IL-6R 1).
GN Name=IL6R;
OS Sus scrofa (Pig);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RA SEQUENCE FROM N.A.
RA Morris K.R., Strom A.D.G.;
RT "Cloning and expression of biologically active porcine IL-6 receptor
RT alpha chain."
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 123-186 FROM N.A.
RC TISSUE=Liver;
RA Klier J.V., Matteoli R.L.;
RT "Partial cDNA sequence of porcine interleukin 6 receptor."
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Part of the receptor for interleukin 6. Binds to IL-6
CC with low affinity, but does not transduce a signal. Signal
CC activation necessitate an association with IL6ST. Activation may
CC lead to the regulation of the immune response, acute-phase
CC reactions and hematopoiesis.
CC -1- SUBUNIT: Hexamer of two molecules each of IL6, IL6R and IL6ST (by
CC similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Expressed in liver.
CC -1- DOMAIN: The two fibronectin type III-like domains contained in the
CC C-terminal part form together a cytokine-binding domain.
CC -1- DOMAIN: The WSXWS motif appears to be necessary for proper protein

```

```

CC folding and thereby efficient intracellular transport and cell-
CC surface receptor binding.
CC -1- SIMILARITY: Belongs to the type I cytokine family of receptors.
CC Subfamily 3.
CC -1- SIMILARITY: Contains 1 fibronectin type III domain.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb.ch/announce/
CC or send an email to license@isb.ch).
CC
DR EMBL: AF147881; AAF73109.1; -.
DR EMBL: AF015116; AAB70916.1; -.
DR HSSP: P08887; IN26.
DR InterPro: IPR002996; Cytokn_recept_B/G.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR008957; FN_III-like.
DR InterPro: IPR003530; Hemtrecept_L_F3.
DR InterPro: IPR007110; Ig-like.
DR Pfam: PF00047; Ig; 1.
DR PROSITE: PS50853; FN3; 1.
DR PROSITE: PS01354; HEMATOPO_REC_L_F3; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
KW Glycoprotein; Immunoglobulin domain; Receptor; Signal; Transmembrane.
FT CHAIN 1 19
FT DOMAIN 20 467
FT TRANSMEM 366 386
FT DOMAIN 387 467
FT DOMAIN 20 112
FT SITE 303 307
FT DISULFID 25 193
FT DISULFID 47 96
FT DISULFID 121 132
FT DISULFID 165 176
FT CARBOHYD 55 55
FT CARBOHYD 93 93
FT CARBOHYD 221 221
FT CARBOHYD 350 350
SQ SEQUENCE 467 AA; 51066 MW; A2B0B884EF21C502 CRC64;

Query Match 51.3%; Score 1468; DB 1; Length 467;
Best Local Similarity 75.1%; Pred. No. 5,7e-95;
Matches 280; Conservative 27; Mismatches 58; Indels 8; Gaps 1;

QY 1 MLAVGALLAALAAFGAALAPRCPAEOVARGVLTSLPDGSLTLTCGVEPNDNTVM 60
DB 1 MLAVGALLAALAAFGAALAPRCPAEOVARGVLTSLPDGSLTLTCGVEPNDNTVM 60
QY 61 VLKRPAGSHPSWAGMGRRLILRSVQLHDSGNYSCYRAGRPAQVHLVDPVEEPOLS 120
DB 61 VLKRPAGSHPSWAGMGRRLILRSVQLHDSGNYSCYRAGRPAQVHLVDPVEEPOLS 120
QY 121 CFRKSPLSNVVCGWGRSTPSLTTKAVLVKRFQNSPAEDFOBPCCOYSQSFSCQLAV 180
DB 121 CFRKSPLSNVVCGWGRSTPSLTTKAVLVKRFQNSPAEDFOBPCCOYSQSFSCQLAV 180
QY 181 PEGDSSFYIVSMCVASSVSGSKFQTFQCGILQDPDPANITVTVANRPRMLSTWOD 240
DB 181 PEGDSSFYIVSMCVASSVSGSKFQTFQCGILQDPDPANITVTVANRPRMLSTWOD 240
QY 241 PHSWNSFYRLRPELRYRERSKFTTMMVKDQHCVIDHWSGLRHVVQLRAQEFQ 300
DB 241 PHSWNSFYRLRPELRYRERSKFTTMMVKDQHCVIDHWSGLRHVVQLRAQEFQ 300
QY 301 GEMSESPKAMGTPWTESSPPAENEVSTPMQALTNKDDNILFRDSANATSLPYEFMP 360
DB 301 GEMSESPKAMGTPWTESSPPAENEVSTPMQALTNKDDNILFRDSANATSLPYEFMP 360

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----- 356

RESULT 3
IL6A RAT
STANDARD
PRT: 462 AA.

AC P12275;1991 (Rel. 19, Created) (IL-6R 1.)
 DT 01-AUG-1991 (Rel. 31, Last sequence update)
 DT 01-FEB-1995 (Rel. 44, Last annotation update) (IL-6R 1.)
 DT 05-JUL-2004 (Rel. 44, Last annotation update) (IL-6R 1.)
 DE Interleukin-6 receptor alpha chain precursor
 GN Name=IL6r;
 GN Name=norvegicus (Rat).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
 OC NCBI_TaxID=10116;
 OX

RP SEQUENCE FROM N.A.; TISSUE=LIVER;
RC STRAIN=Fischer 344; PubMed:2174054;
RX MEDLINE=9106062; PubMed:2174054;
RA Baumann M., Baumann H., "Characterization and functional expression of the
RT "Molecular cloning, characterization and functional expression of the
RT rat liver intercalin 6 receptor".
J. Biol. Chem. 265:11953-11962(1990).
RN [2] CHARACTERIZATION OF PROBABLE FRAMESHIFT IN 227-261.

```

RA  Gasbón 1995.
RL  Unpublished observations (FEB-1995).
CC  -1- FUNCTION: Part of the receptor for interleukin 6. Binds to IL-6
CC  with low affinity, but does not transduce a signal. Signal
CC  activation necessitates an association with IL6ST. Activation may
CC  lead to the regulation of the immune response, acute-phase
CC  reactions and hematopoiesis.
CC  -1- SUBUNIT: Hexamer of two molecules each of IL6, IL6R and IL6ST (by
CC  similarity).
CC  -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC  -1- DOMAIN: The two fibronectin type III-like domains contained in the
CC  C-terminal part form together a cytokine-binding domain.
CC  -1- DOMAIN: The WSXWS motif appears to be necessary for proper cell-
CC  folding and thereby efficient intracellular transport and cell-
CC  surface receptor binding.
CC  -1- SIMILARITY: Belongs to the type I cytokine family of receptors.
CC  -1- Subfamily 3.
CC  -1- SIMILARITY: Contains 1 fibronectin type III domain.
CC  -1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
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CC      or send an email to cc@hpc.nih.gov
CC      -----
DR      EMBL, M58587; AAA41431.1; -.
DR      PIR, A37986; A37986.
DR      HSSP, P08887; 1N26.
DR      RGD, 2902; 116r.
DR      InterPro, IPR002986; Cytkn_recept_B/G.
DR      InterPro, IPR003961; FN_II.
DR      InterPro, IPR008957; FN_II-1like.
DR      InterPro, IPR003530; HemptreceptL_F3.
DR      InterPro, IPR007110; Ig-1like.
DR      Pfam, PRF00641; fn3; 1.
DR      Pfam, PF00647; fn3; 1.
DR      PROSITE, PS50853; FN3; 1.
DR      PROSITE, PS01353; HEMATOPO_REC_L_F3; 1.
DR      PROSITE, PS50833; IG_LIKE; 1.
DR      Glycoprotein, Immunoglobulin domain; Receptor; Signal; Transmembrane.
KW

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FT	SIGNAL	1	19
FT	CHAIN	2	462
FT	DOMAIN	20	364
FT	TRANSMEM	365	385
FT	DOMAIN	386	462
FT	DOMAIN	20	108
FT	DOMAIN	213	308
FT	DOMAIN	404	408
FT	SITE	300	304
FT		25	190
FT	DISUFRD	47	92
FT	DISUFRD	117	178
FT	DISUFRD	162	123
FT	CARBOHYD	32	55
FT	CARBOHYD	5	85
FT	CARBOHYD	85	150
FT	CARBOHYD	150	261
FT	CONFLICT	227	

Ref. 1)

SEQUENCE 462 AA; 50398 MW; AAD6064CRDC0537D CRC64;

001... DR 1: Length 462;

Query Match	34.6%;	Score 931;	20	61
Best Local Similarity	52.9%;	Pred. No. 2.3e-61		
Matches 194;	Conservative	51;	Mismatches 112;	Indels 10;
				Gaps 6;
QY	1	MLAVGALLAALLAAGALAAAPRCACDAEVARGVLTSPGDSVTLTCGVEEDENATVHM	60	
Db	1	MLAVGCTLLAALLAAPRVALLVGLSCRALEFANGVTVSLPGATVTLICPEKELAAGNATIHM	60	
QY	61	VLRKPAAGSHPSRWAGKGRLLRSVQJHDSGNYSCYRAGRPAAGTIVHLLVDVPEEPQLS	120	
Db	61	VY-----SSGSQRSEWTTTGNTLVLAFAVANDTGHILEFDHDLVGTVPLLVDVPEEPKLS	116	
QY	121	CFRRKPLSNVVCWCGPRSTPSLTITKAVLLVRFKFPNSPAE-DPQEPQYSGSGKFCSCOLA	179	
Db	117	CFRRKPLVNAFCEHPSSTPSPTTKAVMFAKINTTGKSDFOVPCQYSGQLKSFSGEVE	176	
QY	180	VEPGDSSEFYIVSMCVASVSGKFKETQFPGCGILQDPDPANITVTVAANRPMWLSWTQ	239	
Db	177	ILLEGDVYHIVLCAVNSVGSRSSNNVVFQSLKRWQDPDPANILVVAIIPGXPMVLKVSWQ	236	
QY	240	DPSNNSSSPYRLRFELRYFAERSKTFITVMVKDLOLHCVCVHDVAGSARHVVLQAOEEFG	299	
Db	237	DPSMPSSTILLOFELRYRPMWSKKFTWPLDVAOHCVIHDALRGVHVVQVSGKEEFD	296	
QY	300	QGESEWSEPMAGCTPW-TESRSPPAENEVSTPMOALLTNKDDNILLFSDSANAISTL--FY	356	
Db	297	IGQSSKMSPEVGTGPMILAEPRITPA-GTGNPLQYSEVEDYDNEHQYSGSSTEATISVLAPV	351	
QY	357	E-FMFPVP	362	
Db	356	QGSSTFP	362	

RESULT 4			
ID	IL6A MOUSE	STANDARD:	PRT: 460 AA.
IL6A_MOUSE			
AC	P22272;		
DC	01-AUG-1991 (Rel. 19, Created)		
DT	01-AUG-1992 (Rel. 23, Last sequence update)		
DT	05-JUN-2004 (Rel. 44, Last annotation update)		
DT	Interleukin-6 receptor alpha chain precursor (IL-6R-alpha) (II-6R 1).		
DE	Interleukin-6 receptor alpha chain precursor (IL-6R-alpha) (II-6R 1).		
DE	Name: IL6ra; Synonyms: IL6r;		
GN	Name: IL6ra; Synonyms: IL6r;		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	(1)		
RP	SEQUENCE FROM N.A.		
RP	STRAIN=BALE/C; TRISUE=Spleen;		
RC	MEDLINE=9027854; PubMed=211585;		
RA	Sugita T., Totsuka T., Saito M., Yamasaki K., Taga T., Hirano T.,		

RA Kishimoto T.;
 RT "Functional murine interleukin 6 receptor with the intracisternal A
 RT particle gene product at its cytoplasmic domain. Its possible role in
 RT plasmacytogenesis.";
 RL J. Exp. Med. 171:2001-2009(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C3H; TISSUE=Liver;
 RA Fiorillo M.T., Cliberto G., Dente L.;
 RL Submitted (JUL-1990) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Part of the receptor for interleukin 6. Binds to IL-6
 CC with low affinity, but does not transduce a signal. Signal
 CC activation necessitate an association with IL6ST. Activation may
 CC lead to the regulation of the immune response, acute-phase
 CC reactions and hematopoiesis.
 CC -1- SUBUNIT: Hexamer of two molecules each of IL6, IL6R and IL6ST (By
 CC similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- DOMAIN: The two fibronectin type III-like domains contained in the
 CC C-terminal part form together a cytokine-binding domain.
 CC -1- DOMAIN: The WSXWS motif appears to be necessary for proper protein
 CC folding and thereby efficient intracellular transport and cell-
 CC surface receptor binding.
 CC -1- SIMILARITY: Belongs to the type I cytokine family of receptors.
 CC Subfamily 3.
 CC -1- SIMILARITY: Contains 1 fibronectin type III domain.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -----
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 CC or send an email to license@1sb-sib.ch).
 CC -----
 CC EMBL; X51975; CAA36237.1; -;
 CC EMBL; X53802; CAA37810.1; -;
 CC PIR; J01044; J01044.
 CC PIR; J01045; J01045.
 CC HSSP; P08887; IN26.
 CC MGD; MG1:105304; I16ra.
 CC DR InterPro: IPR002996; CytKn recept_B/G.
 CC DR InterPro: IPR003961; FN_III.
 CC DR InterPro: IPR008957; FN_III-like.
 CC DR InterPro: IPR003530; HemprreceptL_F3.
 CC DR InterPro: IPR007110; Ig-1like.
 CC DR Pfam; PF00041; fn3; 1.
 CC DR PROSITE; PS50853; FN3; 1.
 CC DR PROSITE; PS01354; HEMATOPO_REC_L_F3; 1.
 CC DR PROSITE; PS50855; IG_Like; 1.
 CC KW Glycoprotein; Immunoglobulin domain; Receptor; signal; Transmembrane.
 CC FT SIGNAL 1 19
 CC FT CHAIN 20 460
 CC FT DOMAIN 20 364
 CC FT TRANSMEM 365 385
 CC FT DOMAIN 386 460
 CC FT DOMAIN 20 116
 CC FT DOMAIN 213 308
 CC FT DOMAIN 404 408
 CC FT SITE 300 304
 CC FT DISULFID 25 190
 CC FT DISULFID 47 92
 CC FT DISULFID 117 128
 CC FT DISULFID 162 173
 CC FT CARBOHYD 32 32
 CC FT CARBOHYD 55 55
 CC FT CARBOHYD 150 150
 CC FT CONFLICT 374 374
 CC SQ SEQUENCE 460 AA; 50454 MW; F85C5906D08525C4 CRC64;
 Query Match 33.4%; Score 954.5; DB 1; Length 460;

Best Local Similarity 50.1%; Pred. No. 8,5e-59;
 Matches 188; Conservative 52; Mismatches 122; Indels 13; Gaps 5;
 QY 1 MNAVGCALLAALLAAGALARRCPAQAQVAVGLSLPQSDVTLTCRQVPEPDNATVFM 60
 DB 1 MLTVGCTLLVALLAAVAVALVIGSCRALEAVANGVTSLGATVTLCPKEAAGNVTITM 60
 QY 61 YLRKPAAGSPRPMAGMRLLRLRSVQLHDSGYS CYRAGRPAQVTHLLVDVPEEPOLS 120
 DB 61 YV-----SGSQNRNMTTGTNTLVIRVDVQLSDTDGLCSLDHLVGYPLVLDVPEEPKLS 116
 QY 121 CERKSLPNNVCEWGRSPSTLTKAVLLVRKQNSPAE-DPQEPQYQSQESQKFCQLA 179
 DB 117 CRRKNLVNALCEWRSSPTPTKAVLPAAKINTNGKSDQVPCQYQQLKFSQCYE 176
 QY 180 VERGDSFFIVSMCAVSSVGSKFSKQTQGGCIILOPPDPANITVAVANRWLSVTQ 239
 DB 177 ILEGDVYHIVSLCVANSVSKSSSHNEAFHSLKMQDPDPANILVSAIPGRPMLEVSQ 236
 QY 240 DPHSNWSSPYRLRPELRYAERSKPTTMMVVDLOHCVIHDAMSGLRHVYVQLRAQEBG 239
 DB 237 HPEITMDPSTYLLQFQRLRPVMSKETVLLLPVQIQVYIHDALRGVAVVQVRGEBLD 236
 QY 300 QGWSWSESPKAGTPEW-TESRSPAEENEVSTPWQALTTNKDDNILFRSANATSLPVER 358
 DB 297 LGQWSESPKAVGTPIAPRPTTPA-GILMNPQVSEDSANHEDEYESTATSV----- 351
 QY 359 MPVPEGDSKDVAAAP 373
 DB 352 --LAPVQESSMSLSP 364

RESULT 5
 IL6_HUMAN STANDARD; PRT; 212 AA.
 ID IL6_HUMAN
 AC P05231; Q9UCU2; Q9UCU3; Q9UCU4;
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 01-OCT-2004 (Rel. 45, Last annotation update)
 DE Interleukin-6 precursor (IL-6) (B-cell stimulatory factor 2) (BSF-2)
 DE (interferon beta-2) (Hybridoma growth factor) (CTL differentiation
 DE factor) (CDF).
 GN Name=IL6; Synonyms=IFNB2;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCBI TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE=87065033; PubMed=3491332;
 RA Hirano T., Yasukawa K., Harada H., Taga T., Watanabe Y., Matsuda T.,
 RA Kashiyama S.-I., Nakajima K., Koyama K., Iwamatsu A., Tanasawa S.,
 RA Sakiyama F., Matsui H., Takahara Y., Taniguchi T., Kishimoto T.;
 RT "Complementary DNA for a novel human interleukin (BSF-2) that induces
 RT B lymphocytes to produce immunoglobulin.";
 RL Nature 324:73-76(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88082664; PubMed=3500852;
 RA Yasukawa K., Hirano T., Watanabe Y., Muratani K., Matsuda T.,
 RA Nakai S., Kishimoto T.;
 RT "Structure and expression of human B cell stimulatory factor-2 (BSF-
 RT 2/IL-6) gene.";
 RL EMBO J. 6:2939-2945(1987).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87067433; PubMed=3538015;
 RA May L.T., Helfgott D.C., Sehgal P.B.;
 RT "Anti-beta-interferon antibodies inhibit the increased expression of
 RT HLA-B7 mRNA in tumor necrosis factor-treated human fibroblasts:
 RT structural studies of the beta 2 interferon involved.";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:8957-8961(1986).
 RN [4]

SEQUENCE FROM N.A.
MEDLINE=87053818; PubMed=3023045; J.H., Revel M.;
Zilberstein A., Ruggieri R., Korn and genes for human interferon-beta-
"Structure and expression of cDNA and genes for human interferon-beta-
2, a distinct species inducible by growth-stimulatory cytokines.";
EMBO J. 5:2529-2537(1986).
[5]
SEQUENCE FROM N.A.
MEDLINE=88088768; PubMed=3320204; Evers R.F., Pannekoek H.,
Brakenhoff J.P.J., de Groot E.R., Evers R.F., Pannekoek H.,
Aarden L.A.;
"Molecular cloning and expression of hybridoma growth factor in
Escherichia coli.";
J. Immunol. 139:4116-4121(1987).
[6]
SEQUENCE FROM N.A.
MEDLINE=89391958; PubMed=2789513; Matsui H.;
Tonouchi N., Miwa K., Katsuyama H., Matsui H.;
"Deletion of 3' untranslated region of human Bsp-2 mRNA causes
stabilization of the mRNA and high-level expression in mouse NIH3T3
cells.";
Biochem. Biophys. Res. Commun. 163:1056-1062(1989).
[7]
SEQUENCE FROM N.A.
TISSUE=Fibroblast;
MEDLINE=87004683; PubMed=3758081; Derynck R., Tavernier J.,
Haeghebaert G., Content J., Voelckart G., Derynck R., Tavernier J.,
Fiers W.;
"Structural analysis of the sequence coding for an inducible 26-kDa
protein in human fibroblasts.";
Eur. J. Biochem. 159:625-632(1986).
[8]
SEQUENCE FROM N.A.
MEDLINE=8919317; PubMed=3266463; Clark S., Ogawa M.;
Wong G., Witek-Giamotti J., Hewick R., Clark S., Ogawa M.;
"Interleukin 6: identification as a hematopoietic colony-stimulating
factor.";
Mitt. 83:40-47(1988).
[9]
SEQUENCE FROM N.A.
MEDLINE=93178270; PubMed=1291290; Chen O.Y.;
"Stable and efficient expression of human interleukin-6 cDNA in
mammalian cells after gene transfer.";
Chung-Hua Chung Liu Tsa Chih 14:340-344(1992).
[10]
SEQUENCE FROM N.A., AND VARIANTS SER-32 AND VAL-162.
Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,
Nickerson D.A.;
"SeattlegenPE: NHLBI HL66682 program for genomic applications, UW-
PHRC, Seattle, WA (URL: <http://pga.gs.washington.edu>).";
Submitted (JUN-2001) to the EMBL/GenBank/DBS databases.
[11]
SEQUENCE FROM N.A.
TISSUE=Lung;
MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strauberg R.J., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Schenck C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,
Diatchenko L., Soares M.B., Bonaldi M.F., Casavant T.L., Schetz T.E.,
Stapleton M.J., Usdin T.B., Tohivuki S., Carninci P., Prange C.,
Brownstein M.J., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
Boesk S.A., McWen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
Villalón D.K., Muzny D.M., Scdegren E.J., Lu X., Gibbs R.A.,
Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[12]
SEQUENCE OF 30-63.
MEDLINE=88154445; PubMed=3279116; van Damme J., van Beeumen J., Decock B., van Snick J., de Ley M.,
Billiau A.;
"Separation and comparison of two monokines with lymphocyte-activating
factor activity: IL-1 beta and hybridoma growth factor (HGF).
Identification of leukocyte-derived HGF as IL-6.";
J. Immunol. 140:1534-1541(1988).
[13]
SEQUENCE OF 30-50.
MEDLINE=90121567; PubMed=2610854; Ming J.E., Cernetti C., Steinman R.M., Granelli-Piperno A.;
"Interleukin 6 is the principal cytokine for T lymphocyte differentiation
factor for thymocytes in human leukocyte conditioned medium.";
J. Mol. Cell. Immunol. 4:203-211(1989).
[14]
SEQUENCE OF 30-40, AND GLYCOSYLATION.
MEDLINE=91355644; PubMed=1883960; May L.T., Shaw J.E., Khanna A.K., Zabriskie J.B., Sehgal P.B.;
"Marked cell-type-specific differences in glycosylation of human
interleukin-6.";
Cytokine 3:204-211(1991).
[15]
SEQUENCE OF 50-212 OF RECOMBINANT FORM LACKING FIRST DISULFIDE BOND.
MEDLINE=95154344; PubMed=7851440; Berton J., la Flaire A., Bertolero F., Orsini G., Valsasina B.,
Zillicio R., de Filippis V., Polverino de Laureto P., Fontana A.;
"Structure, stability and biological properties of a N-terminally
truncated form of recombinant human interleukin-6 containing a single
disulfide bond.";
Eur. J. Biochem. 227:573-581(1995).
[16]
DISULFIDE BONDS.
MEDLINE=92826115; PubMed=2472117; Clogston C.L., Boone T.C., Grandall B.C., Mendiaz E.A., Lu H.S.;
"Disulfide structures of human interleukin-6 are similar to those of
human granulocyte colony stimulating factor.";
Arch. Biochem. Biophys. 272:114-151(1989).
[17]
MUTAGENESIS.
MEDLINE=91243808; PubMed=2037043; Luetjens C., Krieger A., Moeller C., Heinrich P.C., Rose-John S.;
"Evidence for the importance of a positive charge and an alpha-helical
structure of the C-terminus for biological activity of human IL-6.";
FEBS Lett. 282:265-267(1991).
[18]
STRUCTURE BY NMR.
MEDLINE=96134845; PubMed=8555185; Nishimura C., Matsumoto A., Gonda H., Shimada I., Arata Y.;
"Folding topologies of human interleukin-6 and its mutants as studied
by NMR spectroscopy.";
Biochemistry 35:273-281(1996).
[19]
STRUCTURE BY NMR.
MEDLINE=97303053; PubMed=9159484; Xu G.-Y., Yu H.-A., Hong J., Stahl M., McDonagh T., Kay L.E.,
Cumming D.A.;
"Solution structure of recombinant human interleukin-6.";
J. Mol. Biol. 268:468-481(1997).
[20]
X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
MEDLINE=97224126; PubMed=9118960; Somers W., Stahl M., Seehra J.S.;
"1.9-A crystal structure of interleukin 6: implications for a novel
mode of receptor dimerization and signaling.";
EMBO J. 16:989-997(1997).
-1- FUNCTION: IL-6 is a cytokine with a wide variety of biological
functions: it plays an essential role in the final differentiation
of B-cells into Ig-secreting cells, it induces myeloma and

plasmacytoma growth, it induces nerve cells differentiation, in hepatocytes it induces acute phase reactants.

CC - SUBCELLULAR LOCATION: Secreted.

CC - PTM: N- and O-glycosylated.

CC - SIMILARITY: Belongs to the IL-6 superfamily.

CC - DATABASE: NAME=RD Systems' cytokine mini-reviews: IL6; WWW="http://www.rndsystems.com/asp/g_sitbuilder.asp?bodyId=208".

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Query Match 32.8%; Score 938.5; DB 1; Length 212;
Best Local Similarity 97.9%; Pred. No. 4e-58;
Matches 187; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 354 LPVEF-MPVPGEDSKDVAAPHROPITSSERIDKQIRYILDGISALRKETCKNSNMCESS 412
Db 22 LPAAFPAPVPBGEDSKDVAAPHROPITSSERIDKQIRYILDGISALRKETCKNSNMCESS 81

QY 413 KEALAENNINLPRMAEKDSCFSGFNEETCLVKITITGLLEFEVYLEYLONRFESSSEQR 472
Db 82 KEALAENNINLPRMAEKDSCFSGFNEETCLVKITITGLLEFEVYLEYLONRFESSSEQR 141

QY 473 AVQWSTKVLIOFLQKAKKLDIAITTPDPTTNASLITKLOAQONQWLODMTHILIRSFKEF 532
Db 142 AVQWSTKVLIOFLQKAKKLDIAITTPDPTTNASLITKLOAQONQWLODMTHILIRSFKEF 201

QY 533 LQSSLRALRQW 543
Db 202 LQSSLRALRQW 212

RESULT 6
AAS07539 PRELIMINARY; PRT; 212 AA.

AC AAS07539; (TRENBLREL. 27, Created)
DT 02-MAR-2004 (TRENBLREL. 27, Last sequence update)
DT 02-MAR-2004 (TRENBLREL. 27, Last annotation update)
DE Hypothetical protein IL6.
GN IL6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22737999; PubMed=12853948;
RA Hillier L.W., Fulton R.S., Fulton L.A., Graves T.A., Pepin K.H., Wagner-McPherson C., Layman D., Maas J., Jaeger S., Walker R., Wylie K., Sekhon M., Becker M.C., O'Laughlin M.D., Schaller M.E., Sun H., Edwards J., Bradshaw-Cordun H., Ali J., Andrews S., Isak A., Vandrunen A., Nguyen C., Du F., Lamar B., Courtney L., Kalicki J., Ozersky P., Bielicki L., Scott K., Holmes A., Harkins R., Harris A., Strong C.M., Hou S., Tomlinson C., Dauphin-Kohlberg S., Kozlowicz-Cham M.T., Leonard S., Rohlfing T., Rock S.M., Tin-Wollam A.M., Abbott A., Mink P., Maupin R., Strommatt C., Latreille P., Miller N., Johnson D., Morley J., Woessner J.P., Wendl M.C., Yang S.P., Schultz B.R., Wallis J.W., Spieeth J., Bieri T.A., Nelson J.O., Berkowicz N., Wohlmann P.E., Cook L.L., Hickenbotham W.T., Eldred J., Williams D., Bedell J.A., Mardis E.R., Clifton S.W., Chisoe S.L., Marra M.A., Raymond C., Haugen E., Gillet W., Zhou Y., James R., Phelps K., Iadonoto S., Bub K., Simme E., Levy R., Clendenning J., Kaut R., Kent W.J., Furey T.S., Baerisch R.A., Brent M.R., Keibler E., Filcek P., Bork P., Suyama M., Bailey J.A., Portnoy M.E., Torrente D., Chinwalla A.T., Gish W.R., Eddy S.R., McPherson J.D., Olson M.V., Eichler E.E., Green E.D.,

Waterston R.H., Wilson R.K.;
RT "The DNA sequence of human chromosome 7."; Nature 424:157-164 (2003).
RN [2]
RP SEQUENCE FROM N.A.
RA Haekenson W., Nguyen C., Yoakum M.;
RT "The sequence of Homo sapiens BAC clone RP11-240H8."; Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Waterston R.H.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Waterston R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA Wilson R.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC073072; AAS07539.1; -
KW Hypothetical protein.
SQ SEQUENCE 212 AA; 23718 MW; 1F1ED1FE1B734079 CRC64;

Query Match 32.8%; Score 938.5; DB 2; Length 212;
Best Local Similarity 97.9%; Pred. No. 4e-58;
Matches 187; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 354 LPVEF-MPVPGEDSKDVAAPHROPITSSERIDKQIRYILDGISALRKETCKNSNMCESS 412
Db 22 LPAAFPAPVPBGEDSKDVAAPHROPITSSERIDKQIRYILDGISALRKETCKNSNMCESS 81

QY 413 KEALAENNINLPRMAEKDSCFSGFNEETCLVKITITGLLEFEVYLEYLONRFESSSEQR 472
Db 82 KEALAENNINLPRMAEKDSCFSGFNEETCLVKITITGLLEFEVYLEYLONRFESSSEQR 141

QY 473 AVQWSTKVLIOFLQKAKKLDIAITTPDPTTNASLITKLOAQONQWLODMTHILIRSFKEF 532
Db 142 AVQWSTKVLIOFLQKAKKLDIAITTPDPTTNASLITKLOAQONQWLODMTHILIRSFKEF 201

QY 533 LQSSLRALRQW 543
Db 202 LQSSLRALRQW 212

RESULT 7
CAG29292 PRELIMINARY; PRT; 212 AA.

ID CAG29292;
DT 20-MAY-2004 (TRENBLREL. 27, Created)
DT 20-MAY-2004 (TRENBLREL. 27, Last sequence update)
DT 20-MAY-2004 (TRENBLREL. 27, Last annotation update)
DE IL6 protein (Fragment).
GN IL6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Ebert L., Schick M., Neubert P., Schatten R., Henze S., Korn B.;
RT "Cloning of human full open reading frames in Gateway(TM) system entry RT Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: CR450296; CAG29292.1; -
FT NON TER 212
SQ SEQUENCE 212 AA; 23718 MW; 1F1ED1FE1B734079 CRC64;

Query Match 32.8%; Score 938.5; DB 2; Length 212;
Best Local Similarity 97.9%; Pred. No. 4e-58;
Matches 187; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 354 LPVEF-MPVPGEDSKDVAAPHROPITSSERIDKQIRYILDGISALRKETCKNSNMCESS 412

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Db      22 LPAAFPAYVPGDESKDVAAEPHROPITSSSERIDKQIRVIYIDG;SARKETCNKSMCCS 81
Qy      413 KEALAENNINLPKNAEKDGCFCOSGNETCLVKITIGLFEFVLEYLTONRFPSSSEQR 472
Db      82 KEALAENNINLPKNAEKDGCFCOSGNETCLVKITIGLFEFVLEYLTONRFPSSSEQR 141
Qy      473 AVONSTKVLIOFLQKKAKNLDATITPTDPTNASLITLQLOONCLODMTHLILRSFKFR 532
Db      142 AVONSTKVLIOFLQKKAKNLDATITPTDPTNASLITLQLOONCLODMTHLILRSFKFR 201
Qy      533 LOSSLRALROM 543
Db      202 LOSSLRALROM 212

RESULT 8
IL6_MACFA STANDARD; PRT; 212 AA.
ID IL6_MACFA
AC P79341;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interleukin-6 precursor (IL-6).
GN Name=IL6;
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey);
OC Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopithecinae; Macaca.
OC NCBI_TaxID=9541;
OX [1]
RN SEQUENCE FROM N.A.
RA Tasumi M.;
RT Molecular cloning and expression of cynomolgus monkey interleukin-
6."
Submitted (JAN-1997) to the EMBL/Genbank/DBJ databases.
-1- FUNCTION: IL-6 is a cytokine with a wide variety of biological
functions: it plays an essential role in the final differentiation
of B-cells into Ig-secreting cells, it induces myeloma and
plasmacytoma growth, it induces nerve cells differentiation, in
hepatocytes it induces acute phase reactants (By similarity).
-1- SUBCELLULAR LOCATION: Secreted.
-1- SIMILARITY: Belongs to the IL-6 superfamily.
-----
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CC CC
CC EMBL; AB000554; BAA19148.1; -.
CC HSSP; P05231; IL6.
CC InterPro; IPR009079; 4_helix_cytokine.
CC InterPro; IPR003573; IL6_MGF_GCSF.
CC InterPro; IPR003574; Interleukin_6.
CC Pfam; PF00489; IL6; 1.
CC PRINTS; PR00433; IL6GCSFMGF.
CC PRINTS; PR00434; INTERLEUKIN6.
CC ProDom; PD004356; Interleukin_6.
CC SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
DR Acute phase; Cytokine; Glycoprotein; Growth factor; Signal.
KM SIGNAL 1 29
FT CHAIN 30 212
FT DISULFID 72 78
FT DISULFID 101 111
FT CARBOHYD 73 73
FT CARBOHYD 172 172
SQ SEQUENCE 212 AA; 23654 MW; CFB173FCBF0B0389 CRC64;

31.7%; Score 907.5; DB 1; Length 212;

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Best Local Similarity	94.8%	Pred No. 6.1e-56;	Matches 181;	Conservative	3;	Mismatch	6;	Indels	1;	Gap	1;
QY	354	LPEVF-MPVPGEGSKVNA	PHRQPLTSSERIDKQIRYLIDGISALRKETCNKSNVCESS								412
Db	22	LPAAPPAVALPGEESKVNA	PHSQPLTSSSRIDKHIRYLIDGISALRKETCNKSNVCESS								81
QY	413	KEALAENNINLPKNAE	HDGCGSGFNETGCVKILITGLLEFEVYLEYIONRPPSSFEQAR								472
Db	82	KEALAENNINLPKNAE	KDGCFCGSGFNEDTGVKILITGLLEFEVYLEYIONRPPSSFEQAR								141
QY	473	AVQMSKVLVIOFLQKKA	KNLPAITTPPTPTNASTLTQLQANOMLODMTHLILRSFKEF								532
Db	142	AVQMSKVLVIOFLQKKA	KNLPAITTPPTPTNASTLTQLQANOMLODMTHLILRSFKEF								201
QY	533	LOSSIRALRQRM		543							
Db	202	LOSSIRALRQRM		212							

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RESULT 9
ID IL6 MACMU STANDARD; PRT; 212 AA.
IL6_MACMU
AC PS1494;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interleukin-6 precursor (IL-6).
GN Name:IL6;
OS Macaca mulatta (Rhesus macaque);
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RX MEDLINE=96003435; PubMed=7561102;
RA Villinger F.J., Brar S.S., Mayne A.E., Chikala N., Ansari A.A.;
RT "comparative sequence analysis of cytokine genes from human and nonhuman primates.";
RL J. Immunol. 155:3946-3954(1995).
CC CC -I- FUNCTION: IL-6 is a cytokine with a wide variety of biological functions: it plays an essential role in the final differentiation of B-cells into Ig-secreting cells, it induces myeloma and plasmacytoma growth, it induces nerve cells differentiation, in hepatocytes it induces acute phase reactants (By similarity).
CC CC -I- SUBCELLULAR LOCATION: Secreted.
CC CC -I- SIMILARITY: Belongs to the IL-6 superfamily.
CC CC -----
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CC CC -----
DR EMBL, L26028, AAA9978.1, -.
DR HSSP, PD5231, IAUU.
DR InterPro, IPR009079, 4_helix_cytokine.
DR InterPro, IPR003573, IL6_MGF_GCSP.
DR InterPro, IPR003574, Interleukin_6.
DR Pfam, PF00489, IL6, 1.
DR PRINTS, PR00433, IL6GCSFMPF.
DR PRINTS, PR00434, INTERLEUKIN6.
DR ProDom, PD004356, Interleukin_6, 1.
DR SMART, SM00126, IL6, 1.
DR PROSITE, PS00254, INTERLEUKIN_6, 1.
KW Acute phase; Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 29 By similarity.
FT CHAIN 30 212 Interleukin-6.
FT DISULFID 72 78 By similarity.
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FT DISULFID 101 111 By similarity.
FT CARBOHYD 73 73 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 172 172 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 212 AA; 23728 MW; 4130DF0CF0BCAD CRC64;

Query Match
Best Local Similarity 31.4%; Score 899.5; DB 1; Length 212;
Matches 179; Conservative 5; Mismatches 6; Indels 1; Gaps 1;

QY 354 LVEF-MPVPGSDSDVAAPHQPLTSEBRIDKQIRYILDGSAKRTCKNSNCCSS 412
DB 22 LPAAPAPVLPBGSDSKVAAPHQPLTSSBRIDKIRYILDGSAKRTCKNSNCCSS 81

QY 413 KEALAENNINLPKMAEKDCFCGSGFNEETCLVKIITGLLEFVYLYEQNRFSSSEQAR 472
DB 82 KEALAENNINLPKMAEKDCFCGSGFNEETCLVKIITGLLEFVYLYEQNRFSSSEQAR 141

QY 473 AVQWSTKVLIOFLQKAKKLDATITPDPPTNNSLTKLOAQONQWLODMTHILRSFKEF 532
DB 142 AVQWSTKVLIOFLQKAKKLDATITPDPPTNNSLTKLOAQONQWLODMTHILRSFKEF 201

QY 533 LOSSLRALROM 543
DB 202 LOSSLRALROM 212

RESULT 10
QY 097540 PRELIMINARY; PRT; 209 AA.
AC 097540;
DT 01-MAY-1999 (TEMBLrel. 10, Created)
DT 01-MAY-1999 (TEMBLrel. 10, Last sequence update)
DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
DE Interleukin-6 (Fragment).
GN Name=IL-6;
OS Aotus nancyanae (Maca's night monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
OX NCBI_Taxid=37293;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22354194; PubMed=12466897;
RA Hernandez B.C., Suarez C.F., Mendez J.A., Echeverry S.J.,
RA Murillo L.A., Pararoyo M.E.;
RT "Identification, cloning, and sequencing of different cytokine genes
in four species of owl monkey."
RL Immunogenetics 54:645-653(2002).
DR GO; GO:0005176; C:extracellular; IBA.
DR GO; GO:0005125; F:cytokine activity; IBA.
DR GO; GO:0005138; F:interleukin-6 receptor binding; IBA.
DR GO; GO:0006955; P:immune response; IBA.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR InterPro; IPR003574; Interleukin_6.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GSGMFG.
DR PRINTS; PR00434; INTERLEUKIN6.
DR PRODOM; PD004356; Interleukin_6; 1.
DR SMART; SM00126; IL6; 1.
DR SMART; SM00254; INTERLEUKIN_6; 1.
FT NON_TER 1
FT NON_TER 209
SQ SEQUENCE 209 AA; 23406 MW; E84F085DD84002DD CRC64;

Query Match
Best Local Similarity 31.4%; Score 898.5; DB 2; Length 209;
Matches 178; Conservative 5; Mismatches 4; Indels 1; Gaps 1;

QY 354 LVEF-MPVPGSDSDVAAPHQPLTSSBRIDKQIRYILDGSAKRTCKNSNCCSS 412
DB 22 MPAAFPAPVLPBGSDSKVAAPHQPLTSSBRIDKIRYILDGSAKRTCKNSNCCSS 81

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QY 413 KEALAENNINLPKMAEKDCFCGSGFNEETCLVKIITGLLEFVYLYEQNRFSSSEQAR 472
DB 82 KEALAENNINLPKMAEKDCFCGSGFNEETCLVKIITGLLEFVYLYEQNRFSSSEQAR 141

QY 473 AVQWSTKVLIOFLQKAKKLDATITPDPPTNNSLTKLOAQONQWLODMTHILRSFKEF 532
DB 142 AVQWSTKVLIOFLQKAKKLDATITPDPPTNNSLTKLOAQONQWLODMTHILRSFKEF 201

QY 533 LOSSLRAL 540
DB 202 LOSSLRAL 209

RESULT 11
QY IL6_CERTO STANDARD; PRT; 212 AA.
AC P46650;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interleukin-6 precursor (IL-6).
GN Name=IL6;
OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercopithecus.
OX NCBI_Taxid=9531;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FUJ;
RX MEDLINE=96003435; PubMed=7561102;
RA Villinger F.J., Brar S.S., Mayne A.B., Chikkala N., Anasari A.A.;
RT "Comparative sequence analysis of cytokine genes from human and
nonhuman primates."
J. Immunol. 155:3946-3954(1995).
RL FUNCTION: IL-6 is a cytokine with a wide variety of biological
functions: it plays an essential role in the final differentiation
of B-cells into Ig-secreting cells, it induces myeloma and
plasmacytoma growth, it induces nerve cells differentiation, in
hepatocytes it induces acute phase reactants.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the IL-6 superfamily.
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CC EMBL; L26032; AAA99972.1; -.
DR HSSP; P05231; IALU.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR InterPro; IPR003574; Interleukin_6.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GSGMFG.
DR PRINTS; PR00434; INTERLEUKIN6.
DR PRODOM; PD004356; Interleukin_6; 1.
DR SMART; SM00126; IL6; 1.
DR SMART; SM00254; INTERLEUKIN_6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
KW Acute phase; Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1
FT CHAIN 30
FT DISULFID 72
FT DISULFID 78
FT CARBOHYD 101
FT CARBOHYD 111
FT CARBOHYD 172
FT CARBOHYD 172
SQ SEQUENCE 212 AA; 23668 MW; C73C035226B44B9F CRC64;

Query Match
Best Local Similarity 31.3%; Score 895.5; DB 1; Length 212;
Matches 178; Conservative 5; Mismatches 4; Indels 1; Gaps 1;

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
OX NCBI_TaxId=57175;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22354194; PubMed=12466897;
RA Hernandez B.C., Suarez C.F., Mendez J.A., Echeverry S.J.,
RA Murillo L.A., Pararoyo M.E.;
RT "Identification, cloning, and sequencing of different cytokine genes
in four species of owl monkey."
RL Immunogenetics 54:645-653 (2002).
DR EMBL; AF097322; AAF21297.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005125; F:cytokine activity; IEA.
DR GO; GO:0005138; F:interleukin-6 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; INTERLEUKIN_6.
DR PRODOM; PD004356; Interleukin_6; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
FT NON TER
SQ SEQUENCE 175 AA; 19205 MW; 2BCCE574CB99B189 CRC64;

Query Match 21.6%; Score 617.5; DB 2; Length 175;
Best Local Similarity 83.8%; Pred. No. 1.3e-35;
Matches 124; Conservative 10; Mismatches 13; Indels 1; Gaps 1;

QY 354 LVEF-MVPPEBDSQVAAPHROPLTSSERIDKOIRYILDGSAKRETCNKNCCSS 412
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
22 MPAAFPAPVPLGDSSEVAAPNRQILTSTQIDKHRIYLEGISLRKETCDNNCCSS 81
QY 413 KEALANNLNLPMAEKDCFOGFEFETCLVKTITGLLEFVYLYLQNRFFESSEQAR 472
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
82 QEALANNLNLPMAEKDCFOGFEFETCLKITTTGLEFVYLYLQNRFFESSKEQAC 141
QY 473 AVQMSKTVLIQFLQKAKNLDAITPDP 500
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
142 AVQMSKTVLIQFLQKAKNLDAITPDP 169
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 15
Q9MYZ7 PRELIMINARY; PRT; 207 AA.
AC Q9MYZ7;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Interleukin-6.
GN Name=IL-6;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxId=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Yoon H.-Y., Shin I.-S.;
RT Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF275796; AAF86275.1; -.
DR HSSP; P05231; IL6.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005125; F:cytokine activity; IEA.
DR GO; GO:0005138; F:interleukin-6 receptor binding; IEA.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR InterPro; IPR003574; Interleukin_6.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; INTERLEUKIN_6.

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DR PRINTS; PR00434; INTERLEUKIN_6.
DR PRODOM; PD004356; Interleukin_6; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
SQ SEQUENCE 207 AA; 23042 MW; 45541AE011C80F50 CRC64;

Query Match 20.2%; Score 577; DB 2; Length 207;
Best Local Similarity 54.5%; Pred. No. 1.1e-32;
Matches 116; Conservative 37; Mismatches 54; Indels 6; Gaps 2;

QY 331 MQALTTNKDDNILEPDSANATSLPVEFMPVPPEBDSQVAAPHROPLTSSERIDKOIRY 390
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 MMSLSTSAFSLGLL---VMATAFP---PGLAGDSKDATSNLSPLTSANKVEBLIKY 54
QY 391 ILDGSAKRETCNKNCCSSKEALANNLNLPMAEKDCFOGFEFETCLVKTITGL 450
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
55 ILGKSLARKKEMCDKFNKCEDSKALANNLNLPMAEKDCFOGFEFETCLVKTITGL 114
QY 451 LFEFVYLYLQNRFFESSEQARAVQMSKTVLIQFLQKAKNLDAITPPTTNASILTKL 510
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
115 VERGLHNLNLQNNYEDKKNVKSVMHSTKILVQMLKSKYKNODEVYTPPTTDAISQAIL 174
QY 511 QAQNMQLQMTHTLLIRSFKEFLQSSLRALROM 543
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
175 QGDEWLKHTTHTLIRSLDEFLQFSLRAVRIM 207

RESULT 16
IL6_PROVI STANDARD; PRT; 209 AA.
ID IL6_PROVI
AC Q28819;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-UTL-2004 (Rel. 44, Last annotation update)
DE Interleukin-6 precursor (IL-6) (Fragment).
GN Name=IL6;
OS Phoca vitulina (Harbor seal).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Pinnipedia; Phocidae; Phoca.
OX NCBI_TaxId=9720;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96163018; PubMed=8575817;
RA King D.P., Schrenzel M.D., McKnight M.L., Reidarson T.H., Hanni K.D.,
RA Stolt J.L., Ferrick D.A.;
RT "Molecular cloning and sequencing of interleukin 6 cDNA fragments from
the harbor seal (Phoca vitulina), killer whale (Orcinus orca), and
Southern sea otter (Enhydra lutris nereis).";
RL Immunogenetics 43:190-195 (1996).
CC -!- FUNCTION: IL-6 is a cytokine with a wide variety of biological
functions: it plays an essential role in the final differentiation
of B-cells into Ig-secreting cells, it induces myeloma and
plasmacytoma growth, it induces nerve cells differentiation, in
hepatocytes it induces acute phase reactants (by similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-6 superfamily.
CC
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or send an email to license@isb-sib.ch).
CC
DR EMBL; LA6802; AAB01430.1; -.
DR HSSP; P05231; IL6.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR InterPro; IPR003574; Interleukin_6.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; INTERLEUKIN_6.
DR PRINTS; PR00434; INTERLEUKIN_6.

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Prodom; PD004356; Interleukin_6; 1.
 DR SMART; SM00126; IL6; 1.
 DR PROSITE; PS00254; INTERLEUKIN_6; 1.
 DR Acute phase; Cytokine; Glycoprotein; Growth factor; Signal.
 KM Acute phase; Cytokine; Glycoprotein; Growth factor; Signal.
 FT NON_TPR 1 1
 FT SIGNAL 26 26 By similarity.
 FT CHAIN 27 209 Interleukin-6.
 FT DISULFID 69 75 By similarity.
 FT DISULFID 98 108 By similarity.
 FT DISULFID 209 AA; 23483 MW; 75144922E43B48E9 CRC64;
 SQ SEQUENCE

Query Match 20.1%; Score 574.5; DB 1; Length 209;
 Best Local Similarity 58.0%; Pred. No. 1.7e-32;
 Matches 112; Conservative 36; Mismatches 42; Indels 3; Gaps 1;

351 ATSLPVEFMVPVPGEDSKDVAAPHROPLTSSERIDKQIRYIIDGIALKRETCNKNCE 410
 20 ATAFPT---PQVGGESQADATSNRPPLTSPDKMEETIKYILGKISALKNEMCKKNCE 76
 411 SSEKALAEENNLPMMAEKDGCFOGSGNEETCLVKIITGLLEFEVYLEYIQNRFESSE 470
 77 DSKEALAEENNLPMMAEKDGCFOGSGNEETCLVKIITGLLEFEVYLEYIQNRFESSE 136
 471 ARAVQNSTVLIQFLQKAKNLDATTPDPTTNASLITKQAOQOMQIDMTTHLILRSFK 530
 137 ANSVYISTKLIVQMLMKVKYSODEVTTPDPTTDSLQAILQADKMLKHTTHILRSLE 196
 531 EFLQSLRALROM 543
 197 DFLQSLRALVRIM 209

RESULT 17
 ID IL6_HORSE STANDARD; PRT; 208 AA.
 AC 095181; 019007; 046568;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Interleukin-6 precursor (IL-6).
 GN Name=IL6;
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OC NCBI_TaxID=9796;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20579380; PubMed=1137120;
 RA Swiderski C.E., Sobol G., Lunn D.P., Horohov D.W.;
 RT "Molecular cloning, sequencing, and expression of equine interleukin-6";
 RT Vet. Immunol. Immunopathol. 77:213-220(2000).
 RL [2]
 RP SEQUENCE FROM N.A.
 RX Leutenegger C.M., Huder J.B., von Rechenberg B., Akens M., Auer J.;
 RT "Molecular cloning of equine interleukin-6";
 RT Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RX lat A.C.K.;
 RT Cloning and expression of equine interleukin-6";
 RT Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: IL-6 is a cytokine with a wide variety of biological
 CC functions: it plays an essential role in the final differentiation
 CC of B-cells into Ig-secreting cells, it induces myeloma and
 CC plasmacytoma growth, it induces nerve cells differentiation, in
 CC hepatocytes it induces acute phase reactants (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the IL-6 superfamily.
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 or send an email to license@sib-sib.ch).

 DR EMBL; U64794; AAB67703.1; -
 DR EMBL; AF005227; AAB62246.1; -
 DR EMBL; AF041975; AAC04574.1; -
 DR PIR; T09216; T09216.
 DR HSP; P05231; IALU.
 DR InterPro; IPR009079; 4 helix_cytokine.
 DR InterPro; IPR003573; IL6_MGF_GCSF.
 DR InterPro; IPR003574; Interleukin_6.
 DR Pfam; PF00489; IL6_1.
 DR PRINTS; PR00433; IL6GSGFMGF.
 DR PRINTS; PR00434; INTERLEUKIN_6.
 DR Prodom; PD004356; Interleukin_6; 1.
 DR SMART; SM00126; IL6; 1.
 DR PROSITE; PS00254; INTERLEUKIN_6; 1.
 DR Acute phase; Cytokine; Glycoprotein; Growth factor; Signal.
 KM Acute phase; Cytokine; Glycoprotein; Growth factor; Signal.
 FT SIGNAL 27 27
 FT CHAIN 26 208 Interleukin-6.
 FT DISULFID 69 75 By similarity.
 FT DISULFID 98 108 By similarity.
 FT CARBOHYD 71 71 N-linked (GLCNAC. . .) (Potential).
 FT CARBOHYD 184 184 N-linked (GLCNAC. . .) (Potential).
 FT CONFLICT 4 5 LS -> FP (in Ref. 1).
 FT CONFLICT 8 8 T -> A (in Ref. 3).
 FT CONFLICT 137 137 I -> V (in Ref. 2).
 FT CONFLICT 205 205 V -> I (in Ref. 3).
 SQ SEQUENCE 208 AA; 23325 MW; A62P4C234056FP66 CRC64;
 Query Match 20.0%; Score 571.5; DB 1; Length 208;
 Best Local Similarity 59.5%; Pred. No. 2.8e-32;
 Matches 113; Conservative 32; Mismatches 41; Indels 7; Gaps 3;

351 ATSLPVEFMVPVPGEDSKDVAAPHROPLTSSERIDKQIRYIIDGIALKRETCNKNCE 410
 23 ATAFPT---PLPGBDETSNGP---LITADTKQHILKIKYILGKISALKNEMCKKNCE 76
 411 SSEKALAEENNLPMMAEKDGCFOGSGNEETCLVKIITGLLEFEVYLEYIQNRFESSE 470
 77 DSKEALAEENNLPMMAEKDGCFOGSGNEETCLVKIITGLLEFEVYLEYIQNRFESSE 136
 471 ARAVQNSTVLIQFLQKAKNLDATTPDPTTNASLITKQAOQOMQIDMTTHLILRSFK 530
 137 IKMQISTKLIVQIMQKMKPE-VTTPDPTNKSILAKHSQEMWLNKTTTHILRSLE 195
 531 EFLQSLRALROM 543
 196 DFLQSLRALVRIM 208

RESULT 18
 ID IL6_ORCOR STANDARD; PRT; 205 AA.
 AC 028747;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Interleukin-6 precursor (IL-6) (Fragment).
 GN Name=IL6;
 OS Oryzias latipes (Zebrafish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Delphinidae;
 OC Oryzias.
 OC NCBI_TaxID=9733;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9616018; PubMed=8575817;
 RA King D.P., Schrenzel M.D., McKnight M.L., Reidarson T.H., Hami K.D.,
 RA Stott J.L., Ferrick D.A.;
 RT "Molecular cloning and sequencing of interleukin 6 cDNA fragments from

RT the harbor seal (*Phoca vitulina*), killer whale (*Orcinus orca*), and
 RT Southern sea otter (*Enhydra lutris nereis*).";
 RL Immunogenetics 43:190-195 (1996).
 CC -I- FUNCTION: IL-6 is a cytokine with a wide variety of biological
 CC functions: it plays an essential role in the final differentiation
 CC of B-cells into Ig-secreting cells, it induces myeloma and
 CC plasmacytoma growth, it induces nerve cells differentiation, in
 CC hepatocytes it induces acute phase reactants (By similarity).
 CC -I- SUBCELLULAR LOCATION: Secreted.
 CC -I- SIMILARITY: Belongs to the IL-6 superfamily.

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 DR EMBL: L46803; AAB01429.1; -.
 DR HSSP: P05231; 1ALU.
 DR InterPro: IPR009079; 4 helix_cytokine.
 DR InterPro: IPR003573; IL6_MGF_GCSF.
 DR InterPro: IPR003574; Interleukin_6.
 DR Pfam: PF00489; IL6; 1.
 DR PRINTS: PR00433; IL6GCSFMGF.
 DR PRINTS: PR00434; INTERLEUKIN_6.
 DR ProDom: PD004356; Interleukin_6; 1.
 DR SMART: SM00126; IL6; 1.
 DR PROSITE: PS00254; INTERLEUKIN_6; 1.
 DR Acute phase; Cytokine; Glycoprotein; Growth factor; Signal.
 FT NON TER 1 1
 FT SIGNAL <1 21 By similarity.
 FT CHAIN 22 205 Interleukin-6.
 FT DISULFID 64 70 By similarity.
 FT DISULFID 93 103 By similarity.
 FT CARBOHYD 164 164 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 205 AA; 23266 MW; 6308F3A457960832 CRC64;
 Query Match 20.0%; Score 571; DB 1; Length 205;
 Best Local Similarity 59.4%; Pred. No. 3e-32;
 Matches 114; Conservative 29; Mismatches 45; Indels 4; Gaps 2;
 QY 351 ATSLPEFMPVPPGEDSKVAAPHROPLTSSERIDKQIRYLLDGISALRKETCKNSMCE 410
 DB 15 ATAFPT---PGPLGDFPKDDTTSRLYLSPPKTEALIKYILGKISAMRKEMCEKDKCE 71
 QY 411 SSKKALANNLNLPKAAEKDGCFOGSGFNEETCLVKIITGLLEFEVLYEVLQNFESSEQ 470
 DB 72 NKKKALANNLNLPKAAEKDGCFOGSGFNEETCLVKIITGLLEFEVLYEVLQNFESSEQ 131
 QY 471 ARAVQSTVLYIQFLQKAKNLDATTPPTTNASILTLKLAQN-OWLODMTHLILRSF 529
 DB 132 IEAVQISSTKALQILRKQKVPDEVTPPTTNASIMNNLQSQNDMDMKTKIILIRSL 191
 QY 530 KEFLQSLRAVR 541
 DB 192 ENFLQPSLRAIR 203
 RESULT 19
 Q9XT80 PRELIMINARY; PRT; 208 AA.
 AC Q9XT80;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Interleukin 6.
 OS Delphinapterus leucas (Beluga whale).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti;
 OC Monocytidae; Delphinapterus.
 OC NCBI_TaxId=9749;

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20141864; PubMed=10678396;
 RA St-Laurent G., Archambault D.,
 RT "Molecular cloning, phylogenetic analysis and expression of beluga
 RT whale (*Delphinapterus leucas*) interleukin 6,"
 RL Vet. Immunol. Immunopathol. 73:31-44 (2000).
 DR EMBL: AF076643; AAD42929.1; -.
 DR HSSP: P05231; 1ALU.
 DR GO: GO:0005576; C:extracellular; IEA.
 DR GO: GO:0005125; F:cytokine activity; IEA.
 DR GO: GO:0005138; F:interleukin-6 receptor binding; IEA.
 DR GO: GO:0006955; P:immune response; IEA.
 DR InterPro: IPR009079; 4 helix_cytokine.
 DR InterPro: IPR003573; IL6_MGF_GCSF.
 DR InterPro: IPR003574; Interleukin_6.
 DR Pfam: PF00489; IL6; 1.
 DR PRINTS: PR00433; IL6GCSFMGF.
 DR PRINTS: PR00434; INTERLEUKIN_6.
 DR ProDom: PD004356; Interleukin_6; 1.
 DR SMART: SM00126; IL6; 1.
 DR PROSITE: PS00254; INTERLEUKIN_6; 1.
 SQ SEQUENCE 208 AA; 23456 MW; 81CC85C6E80389C4 CRC64;
 Query Match 19.6%; Score 562; DB 2; Length 208;
 Best Local Similarity 58.9%; Pred. No. 1.3e-31;
 Matches 113; Conservative 28; Mismatches 47; Indels 4; Gaps 2;
 QY 351 ATSLPEFMPVPPGEDSKVAAPHROPLTSSERIDKQIRYLLDGISALRKETCKNSMCE 410
 DB 18 ATAFPT---PGPLGDFPKDDTTSRLYLSPPKTEALIKYILGKISAMRKEMCEKDKCE 74
 QY 411 SSKKALANNLNLPKAAEKDGCFOGSGFNEETCLVKIITGLLEFEVLYEVLQNFESSEQ 470
 DB 75 NKKKALANNLNLPKAAEKDGCFOGSGFNEETCLVKIITGLLEFEVLYEVLQNFESSEQ 134
 QY 471 ARAVQSTVLYIQFLQKAKNLDATTPPTTNASILTLKLAQN-OWLODMTHLILRSF 529
 DB 135 IEAVQISSTKALQILRKQKVPDEVTPPTTNASIMNNLQSQNDMDMKTKIILIRSL 194
 QY 530 KEFLQSLRAVR 541
 DB 195 ENFLQPSLRAVR 206
 RESULT 20
 IL6_CANFA STANDARD; PRT; 207 AA.
 AC P41323;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Interleukin-6 precursor (IL-6).
 GN Name=IL6;
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OC NCBI_TaxId=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Mongrel;
 RX MEDLINE=94303924; PubMed=7913298;
 RA Kukiela G.L., Youker K.A., Hawkins H.K., Perrard J.L., Michael L.H.,
 RA Ballantyne C.M., Smith C.W., Entman W.L.,
 RT "Regulation of ICM-1 and IL-6 in myocardial ischemia: effect of
 RT reperfusion,"
 RL Ann. N. Y. Acad. Sci. 723:258-270 (1994).
 CC -I- FUNCTION: IL-6 is a cytokine with a wide variety of biological
 CC functions: it plays an essential role in the final differentiation
 CC of B-cells into Ig-secreting cells, it induces myeloma and
 CC plasmacytoma growth, it induces nerve cells differentiation, in
 CC hepatocytes it induces acute phase reactants.
 CC -I- SUBCELLULAR LOCATION: Secreted.

CC -I- SIMILARITY: Belongs to the IL-6 superfamily.
 CC -----
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 CC -----
 CC EMBL: U12234; AAA83030.1; --
 CC HSP: P05231; IL6.
 CC InterPro: IPR009079; 4 helix cytokine.
 CC InterPro: IPR003573; IL6 MGF GCSF.
 CC InterPro: IPR003574; Interleukin_6.
 CC Pfam: PF00489; IL6; 1.
 CC PRINTS: PR00433; IL6GCSFMGF.
 CC PRODOM: PD004356; Interleukin_6; 1.
 CC SMART: SM00126; IL6; 1.
 CC PROSITE: PS00254; INTERLEUKIN_6; 1.
 CC Acute phase; Cytokine; Glycoprotein; Growth factor; Signal.
 CC SIGNAL 1 20 Potential.
 CC CHAIN 1 207 Interleukin-6.
 CC FT DISULFID 67 73 By similarity.
 CC FT DISULFID 96 106 By similarity.
 CC SEQUENCE 207 AA; 22945 MW; 45540154E93C0F50 CRC64;
 SQ
 Query Match 19.6%; Score 561; DB 1; Length 207;
 Best Local Similarity 53.5%; Pred. No. 1.5e-31;
 Matches 114; Conservative 38; Mismatches 55; Indels 6; Gaps 2;
 QY 331 MQALTNNKDDNITLFRDSANATSLPVEFMVPPGSGDSKVAAAPHROPLTSSERIDKOIRY 390
 Db 1 MNSISTAFSLGLL--VNAIAPFL--PGIAGDSKDDATNSLPLTSANKVEELIKY 54
 QY 391 ILDGISALRKETCKNSNMCSSEKALANNLNPRAEKDCCFGSGFNEETCLVYITGL 450
 Db 55 ILGKISALRKEMCKFKCEDSKKALANNLHPKLEKDGCGFSGFNEETCLVITGL 114
 QY 451 LEFEVLEYLONRRESSEBOARAVOMSTKYLIOLOKAKANLDAITTPPTTNASLITKL 510
 Db 115 VEFQIHMLITLONNTEGDEENKSVHMTKILVOMLSKVNQGEVTPPTDASIALTL 174
 QY 511 QAONQWLODMTTHLILRSFKELQSSLRALRQM 543
 Db 175 QSGDECVGHHTIHLIRSLDPLQPSLRARIM 207
 RESULT 21
 IL6 LANGL STANDARD; PRT; 211 AA.
 ID IL6 LANGL
 AC 0865X6;
 DT 29-MAR-2004 (Rel. 43, Created)
 DT 29-MAR-2004 (Rel. 43, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Interleukin-6 precursor (IL-6).
 GN Name=IL6;
 OS Lama glama (Llama).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Lama.
 OC NCB1_TaxID=9844;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Raadan O., Lee S., Yoshida R., Chang K., Ohashi K., Sugimoto C.,
 RA Onuma M.;
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
 RT
 CC -I- FUNCTION: IL-6 is a cytokine with a wide variety of biological
 CC functions: it plays an essential role in the final differentiation
 CC of B-cells into Ig-secreting cells, it induces myeloma and
 CC plasmacytoma growth, it induces nerve cells differentiation, in
 CC hepatocytes it induces acute phase reactants (By similarity).

CC -I- SUBCELLULAR LOCATION: Secreted.
 CC -----
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 CC -----
 CC EMBL: AB107647; BAC75384.1; --
 CC HSP: P05231; IL6.
 CC InterPro: IPR009079; 4 helix cytokine.
 CC InterPro: IPR003573; IL6 MGF GCSF.
 CC InterPro: IPR003574; Interleukin_6.
 CC Pfam: PF00489; IL6; 1.
 CC PRINTS: PR00433; IL6GCSFMGF.
 CC PRODOM: PD004356; Interleukin_6; 1.
 CC SMART: SM00126; IL6; 1.
 CC PROSITE: PS00254; INTERLEUKIN_6; 1.
 CC Acute phase; Cytokine; Growth factor; Signal.
 CC SIGNAL 1 29 Potential.
 CC CHAIN 1 211 Interleukin-6.
 CC FT DISULFID 71 77 By similarity.
 CC FT DISULFID 100 110 By similarity.
 CC SEQUENCE 211 AA; 23988 MW; BB82D263F096B16 CRC64;
 SQ
 Query Match 19.5%; Score 558; DB 1; Length 211;
 Best Local Similarity 56.5%; Pred. No. 2.5e-31;
 Matches 109; Conservative 35; Mismatches 45; Indels 4; Gaps 2;
 QY 351 ATSLPVEEMVPPGSGDSKVAAAPHROPLTSSERIDKOIRYILDGISALRKETCKNSNMCE 410
 Db 23 ATAPFL--PVPLGDFD--GTSKRPTSPDKBELIKILGRISMREKCEKDYKCE 78
 QY 411 SKSEKALANNLNPRAEKDCCFGSGFNEETCLVYITGLLEFEVLEYLONRRESSEBO 470
 Db 79 NSKEALSENNLNPRTKEDCGFSGFNEETCLVITGLLEFEVLEYLONRRESSEBO 138
 QY 471 ARAVOMSTKYLIOLOKAKANLDAITTPPTTNASLITKLQAONQWLODMTTHLILRSFK 530
 Db 139 TEAVQSTVALIOLKOKKQPEEVSTPNITGSSLLAKQTEHQMKNTGMILIRSL 198
 QY 531 EPIQSSLRALRQM 543
 Db 199 DFLOPSLRARIM 211
 RESULT 22
 IL6 LANGL PRELIMINARY; PRT; 211 AA.
 ID 0865W7;
 AC 0865W7;
 DT 01-JUN-2003 (TRENBLREL. 24, Created)
 DT 01-JUN-2003 (TRENBLREL. 24, Last sequence update)
 DT 01-MAR-2004 (TRENBLREL. 26, Last annotation update)
 DE Interleukin 6.
 GN Name=IL-6;
 OS Camelus bactrianus (Bactrian camel).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
 OC NCB1_TaxID=9837;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Raadan O., Lee S., Yoshida R., Chang K., Ohashi K., Sugimoto C.,
 RA Onuma M.;
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
 RT
 CC EMBL: AB107656; BAC75393.1; --
 CC HSP: P05231; IL6.
 CC GO: GO:0005576; C:extracellular; IEA.
 CC GO: GO:0005125; F:cytokine activity; IEA.
 CC GO: GO:0005138; F:interleukin-6 receptor binding; IEA.

DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR009079; 4 helix cytokine.
 DR InterPro; IPR003573; IL6_MGF_GCSF.
 DR InterPro; IPR003574; Interleukin_6.
 DR Pfam; PF00489; IL6; 1.
 DR PRINTS; PR00433; IL6GCSFMGF.
 DR PRINTS; PR00434; INTERLEUKIN6.
 DR ProDom; PD004356; Interleukin_6; 1.
 DR SMART; SM00126; IL6; 1.
 DR PROSITE; PS00254; INTERLEUKIN_6; 1.
 DR SEQUENCE 211 AA; 23929 MW; 0DF8004A16625FE CRC64;
 Query Match 19.5%; Score 558; DB 2; Length 211;
 Best Local Similarity 57.0%; Pred. No. 2.5e-31;
 Matches 110; Conservative 34; Mismatches 45; Indels 4; Gaps 2;
 QY 351 ATSLPVEFWPPGDESKVAAPHROPPLTSSEKIDQRIYLDGIALKRETKNSMCE 410
 DB 23 ATAFPT--PVLGSEDFKGGTTSNR-PFTSPDKSEBLIKYILGRISAMKRECKEKDCE 78
 QY 411 SSKELAENNINLPMKAEKDCGFGSGFNEETCLVKTITGLFEVYLLEYLQNRFESEEQ 470
 DB 79 NSEKALSENNINLPMKTEKDCGFGSGFNETCLMTITGLFEQIYLDVLYQNYEEDKGN 138
 QY 471 ARAVQSTKVLIQFLQKAKNLDATTPPTTNASILTKLQANQWLODMTHLIRSPK 530
 DB 139 TEAVQISTKALIQTLRQKTKQPEVESTPNPTITGSSILNKLTQENQMKTKMLILRSLE 198
 QY 531 EFLQSSLRALROM 543
 DB 199 DFLQFSLRALRIM 211

RESULT 23

IL6_PIG STANDARD; PRT; 212 AA.
 AC P26893; Q95KN6;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Interleukin-6 precursor (IL-6).
 GN Name=IL6;
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 NC NCB1_TaxID=9823;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91338547; PubMed=1873476;
 RA Richard C., Saklatvala J.;
 RT "Molecular cloning and sequence of porcine interleukin 6 cDNA and
 expression of mRNA in synovial fibroblasts in vitro.";
 RL Cytokine 3:269-276 (1991).
 RN (2)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92360284; PubMed=1497880;
 RA Mathias Lagan N., Bixby J.A., Roberts M.R.;
 RT "Expression of interleukin-6 in porcine, ovine, and bovine
 preimplantation conceptuses.";
 RL Mol. Reprod. Dev. 32:324-330 (1992).
 RN (3)
 RP SEQUENCE FROM N.A.
 RC STRAIN=Landrace x Meishan; TISSUE=Blood;
 RA Liu S., Meng M., Gao R.;
 RT "Cloning and expression of interleukin 6 gene from Landrace x Meishan
 hybrid swine.";
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: IL-6 is a cytokine with a wide variety of biological
 functions: it plays an essential role in the final differentiation
 of B-cells into Ig-secreting cells, it induces myeloma and
 plasmacytoma growth, it induces nerve cells differentiation, in
 hepatocytes it induces acute phase reactants.
 CC -!- SUBCELLULAR LOCATION: Secreted.

-!- SIMILARITY: Belongs to the IL-6 superfamily.

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CC EMBL; M86722; AAC37333.1; -.
 CC EMBL; M80258; AAC27127.1; -.
 CC EMBL; AF309651; AAG27730.1; -.
 CC PIR; I46590; I46590.
 CC PIR; I46621; I46621.
 CC HSSP; P05231; IALU.
 DR InterPro; IPR009079; 4 helix cytokine.
 DR InterPro; IPR003573; IL6_MGF_GCSF.
 DR InterPro; IPR003574; Interleukin_6.
 DR Pfam; PF00489; IL6; 1.
 DR PRINTS; PR00433; IL6GCSFMGF.
 DR PRINTS; PR00434; INTERLEUKIN6.
 DR ProDom; PD004356; Interleukin_6; 1.
 DR SMART; SM00126; IL6; 1.
 DR PROSITE; PS00254; INTERLEUKIN_6; 1.
 KW Acute phase; Cytokine; Glycoprotein; Growth factor; Signal.
 FT SIGNAL 1 29 By similarity.
 FT CHAIN 30 212 Interleukin-6.
 FT DISULFID 72 78 By similarity.
 FT DISULFID 101 111 By similarity.
 FT CONFLICT 30 30 E -> G (in Ref. 1).
 SQ SEQUENCE 212 AA; 23952 MW; 1E736FB230B4FC5D CRC64;
 Query Match 19.5%; Score 557.5; DB 1; Length 212;
 Best Local Similarity 57.5%; Pred. No. 2.8e-31;
 Matches 111; Conservative 32; Mismatches 47; Indels 3; Gaps 1;

QY 351 ATSLPVEFWPPGDESKVAAPHROPPLTSSEKIDQRIYLDGIALKRETKNSMCE 410
 DB 23 ATAFPT--PVLGSEDFKGGTTSNR-PFTSPDKSEBLIKYILGRISAMKRECKEKDCE 79
 QY 411 SSKELAENNINLPMKAEKDCGFGSGFNEETCLVKTITGLFEVYLLEYLQNRFESEEQ 470
 DB 80 NSEKALSENNINLPMKTEKDCGFGSGFNETCLMTITGLFEQIYLDVLYQNYEEDKGN 139
 QY 471 ARAVQSTKVLIQFLQKAKNLDATTPPTTNASILTKLQANQWLODMTHLIRSPK 530
 DB 140 TEAVQISTKALIQTLRQKTKQPEVESTPNPTITGSSILNKLTQENQMKTKMLILRSLE 199
 QY 531 EFLQSSLRALROM 543
 DB 200 DFLQFSLRALRIM 212

RESULT 24

08MJ75 PRELIMINARY; PRT; 212 AA.
 AC 08MJ75;
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE IL-6
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 NC NCB1_TaxID=9823;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Lee D., Yoo H., Choi I.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF518322; AAM74938.1; -.
 DR HSSP; P05231; IALU.
 DR GO; GO:0005576; C:extracellular; IEA.

Query	Subject	Score	DB	Length	Gaps
QY	351 ATSLPVEFPPPPEDSDVAAPROPLTSSERIDKQIRYTIIDGISAIRKETCKNSMCE	19.0%	DB 1	208	2
DB	23 ATAFPT---PGPLGSD---ATSNRLPLISADMMELIYILIGKISALRKEMCNVYKCE	55.4%	Pred. No. 2.2e-307	Indels 46	7
QY	411 SSKKALAEENNLPMPEAKKDCGFCGSGNNECTLVKLTIGLAEFEVYLYLONPRESEEO				410
DB	76 DSKKALAEENNLPMPEAKKDCGFCGSGNNECTLVKLTIGLAEFEVYLYLONPRESEEO				135
QY	471 ARAYOMSTKYLQLOKAKAKLDAITTPDDPTTNASLLTKLQANOMLODPTTHLLISFK				530
DB	136 AKSYVYTSITNVLOMKKSKKNDVETIIPVIVEVGLOAKLOSQSEWLRHTTHILTRLE				195
QY	531 EFLQSLRALROM 543				
DB	196 DFLQSLRALVRIM 208				

RESULT 26

097535 PRELIMINARY; PRT; 160 AA.

AC 097535; TREMBLrel. 10, Created (last sequence update)

DT 01-MAY-1999 (TREMBLrel. 10, last annotation update)

DT 01-MAY-1999 (TREMBLrel. 26, last annotation update)

DT 01-MAR-2004 (Fragment).

DE Interleukin-6 (Fragment).

GN Name=IL-6;

OS Acinus vociferans (Spix's owl monkey).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.

OC NCBI_TaxID=57176;

OK

RN

RP SEQUENCE FROM N.A.

RX MEDLINE=22354194; PubMed=12466897;

RA Hernandez E.C., Suarez C.F., Mendez J.A., Echeverry S.J.,

RA Murillo L.A., Patarroyo M.E.;

RT "Identification, cloning, and sequencing of different cytokine genes in four species of owl monkey."

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RL Immunogenetics 54:645-653(2002).
DR EMBL: AF014505; AAD01531.1; -.
DR GO: GO:0005576; C:extracellular; IEA.
DR GO: GO:0005125; F:cytokine activity; IEA.
DR GO: GO:0005138; F:interleukin-6 receptor binding; IEA.
DR GO: GO:0006955; P:immune response; IEA.
DR InterPro: IPR009079; 4 helix_cytokine.
DR InterPro: IPR003573; IL6_MGF_GCSF.
DR InterPro: IPR003574; Interleukin_6.
DR Pfam: PF00489; IL6; 1.
DR PRINTS: PR00433; IL6GCSFMGF.
DR PRODOM: PD004356; Interleukin_6; 1.
DR SMART: SM00126; IL6; 1.
DR PROSITE: PS00254; INTERLEUKIN_6; 1.
FT NON_TER 1 1
SQ SEQUENCE 160 AA; 17855 MW; 07A021338650A46D CRC64;

Query Match 18.9%; Score 539.5; DB 2; Length 160;
Best Local Similarity 84.3%; Pred. No. 3.5e-30;
Matches 107; Conservative 10; Mismatches 9; Indels 1; Gaps 1;

QY 354 LPVPE-MVPVPGEDSKDVAAPHROPLTSSERIDKQIRYILDGISALRKETCNKSNMCESS 412
DB 22 MPAAFPAPVPYLGDSKXVAAPNQLLTSTEQIDKHRIYILEGIALRKETICDKSNMCESS 81
QY 413 KEALANNLNLPRKAEKDCGFCGSGFNEETCLVKIITGLLEFVYLYLQNRFFESSEEO 472
DB 82 KEALANNLNLPRKAEKDCGFCGSGFNEETCLVKIITGLLEFVYLYLQNRFFESSEEO 141
QY 473 AVQVSTK 479
DB 142 AVQVSTK 148

RESULT 27
Q28403 PRELIMINARY; PRT; 207 AA.
AC Q28403;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Interleukin 6 (Fragment).
GN Name=IL-6;
OS Euhadra lutris (Sea otter).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Lutrinae;
OC Euhadra.
OC NCBI_TaxID=34882;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9613018; PubMed=8575817;
RA King D.P., Schrenzel M.D., McKnight M.L., Reidarson T.H., Hanni K.D.,
RA Scott J.L., Ferrick D.A.;
RT "Molecular cloning and sequencing of interleukin 6 cDNA fragments from
RT the harbor seal (Phoca vitulina), killer whale (Orcinus orca), and
RT Southern sea otter (Euhadra lutris nereis).";
RL Immunogenetics 43:190-195(1996).
DR EMBL: L46804; AAB01428.1; -.
DR GO: GO:0005576; C:extracellular; IEA.
DR GO: GO:0005125; F:cytokine activity; IEA.
DR GO: GO:0005138; F:interleukin-6 receptor binding; IEA.
DR InterPro: IPR009079; 4 helix_cytokine.
DR InterPro: IPR003574; Interleukin_6.
DR Pfam: PF00489; IL6; 1.
DR PRINTS: PR00433; IL6GCSFMGF.
DR PRODOM: PD004356; Interleukin_6; 1.
DR SMART: SM00126; IL6; 1.
DR PROSITE: PS00254; INTERLEUKIN_6; 1.
FT NON_TER 1 1

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SQ SEQUENCE 207 AA; 23527 MW; 729E0CD91136D8B CRC64;

Query Match 18.1%; Score 516.5; DB 2; Length 207;
Best Local Similarity 53.9%; Pred. No. 2.1e-28;
Matches 104; Conservative 37; Mismatches 47; Indels 5; Gaps 2;

QY 351 ATSLPVEFMVPVPGEDSKDVAAPHROPLTSSERIDKQIRYILDGISALRKETCNKSNMCESS 410
DB 20 ATAFPT---PGPLGSGSDKDATSNRPPLTSADKMEDEFIKLGKISALRNEMCDKYNKCE 76
QY 411 SSKEALANNLNLPRKAEKDCGFCGSGFNEETCLVKIITGLLEFVYLYLQNRFFESSEEO 470
DB 77 DSKEVLAENNLNLPRKAEKDCGFCGSGFNEETCLVKIITGLLEFVYLYLQNRFFESSEEO 136
QY 471 ARAVQVSTKVLQFLQKAKNLDAITTPDPTNASLITLQANOMLOMTTHLILRSFK 530
DB 137 AHSVYSTHGLQTL--RPANQLEVTTPPTDASLQALFKSDQKWLKHTHILRLR 194
QY 531 EFLQSSLRALRQW 543
DB 195 DFLQPSLRALRIM 207

RESULT 28
Q8MKES PRELIMINARY; PRT; 214 AA.
AC Q8MKES;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Interleukin-6.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OC NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Wu M., Gao R., Li J., Meng M., Long Z., Tang M., Liu S.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF493992; AAM27192.1; -.
DR HSSP: P05231; 1ALU.
DR GO: GO:0005576; C:extracellular; IEA.
DR GO: GO:0005125; F:cytokine activity; IEA.
DR GO: GO:0005138; F:interleukin-6 receptor binding; IEA.
DR GO: GO:0006955; P:immune response; IEA.
DR InterPro: IPR009079; 4 helix_cytokine.
DR InterPro: IPR003573; IL6_MGF_GCSF.
DR InterPro: IPR003574; Interleukin_6.
DR Pfam: PF00489; IL6; 1.
DR PRINTS: PR00433; IL6GCSFMGF.
DR PRODOM: PD004356; Interleukin_6; 1.
DR SMART: SM00126; IL6; 1.
DR PROSITE: PS00254; INTERLEUKIN_6; 1.
SQ SEQUENCE 214 AA; 23765 MW; 50849FB040DBD7F CRC64;

Query Match 17.5%; Score 501.5; DB 2; Length 214;
Best Local Similarity 57.3%; Pred. No. 2.5e-27;
Matches 98; Conservative 28; Mismatches 36; Indels 9; Gaps 2;

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QY 351 ATSLPVEFMVPVPG---EDSKDVAAPHROPLTSSERIDKQIRYILDGISALRKETCNKSN 407
DB 23 ATAFPT-----DRLSEDDKGDATSDKMLFTSPDTEELIKYILGKISAMRKECKEYK 76
QY 408 MCSSEKALANNLNLPRKAEKDCGFCGSGFNEETCLVKIITGLLEFVYLYLQNRFFESS 467
DB 77 KCNSKEVLAENNLNLPRKAEKDCGFCGSGFNEETCLVKIITGLLEFVYLYLQNRFFESS 136
QY 468 BEQARAQVQSTKVLQFLQKAKNLDAITTPDPTNASLITLQANOMLOMTTHLILRSFK 518
DB 137 KGNVAEAVQISTKALITLQKRGKGNPKATTPNPTNAGLGLDKLQSONEMWK 187

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RESULT 29
Q6OHY3 PRELIMINARY; PRT; 191 AA.
ID Q6OHY3
AC Q6OHY3;
DT 05-JUL-2004 (TREMblrel. 27, Created)
DT 05-JUL-2004 (TREMblrel. 27, Last sequence update)
DE Interleukin-6 (Fragment).
OS Cervus elaphus (Red deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae;
OC Cervinae; Cervus.
OX NCBI_TaxID=9860;
RN [1]
RP SEQUENCE FROM N.A.
RA O'Brien R., Berger S., Griffin F.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY540191; AAS73282.1; -.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR InterPro; IPR003574; Interleukin_6.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR PRINTS; PR00434; INTERLEUKIN6.
DR PRODOM; PD004356; Interleukin_6; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
FT NON TER 1 191
SQ SEQUENCE 191 AA; 21677 MW; 5936607DB4D3C1A0 CRC64;

Query Match 16.9%; Score 482.5; DB 2; Length 191;
Best Local Similarity 49.7%; Pred. No. 4.6e-26;
Matches 95; Conservative 40; Mismatches 49; Indels 7; Gaps 3;

QY 349 ANATSLVEFMPVPEDSKVAAPHROPLTSSERIDKQIRYLIDGIALRKETCKNSNM 408
DB 8 AMASAPFT---PGLGEDPKNDTPPSRLITTPKTEALIKHIVDKISARKKEICEKNDK 64
QY 409 CESSKEALANNINLPMKAEKDCGFCGSGFNETCLVKIITGLIEFEVYLEYLNRFSSSE 468
DB 65 CENSKETLAENNINLPMKKEKDCGFCGSGFNETCLIRSTVGLLEYQTYLDYLNQNEYEGDQ 124
QY 469 EQRNAVQMSKTVLIQLOKAKKRLDATTPTPTNASLITLQAOQNOIMQDMTHILRS 528
DB 125 ENVKDLRSSIRTLQIMRQ--KSIDLVT--ATTNPDLERKQSSNEWVKNAKIILIRS 180
QY 529 FKEFLQSSLR 539
DB 181 LENFLQPSLR 191

RESULT 30
AAS73282 PRELIMINARY; PRT; 191 AA.
ID AAS73282
AC AAS73282;
DT 29-MAR-2004 (TREMblrel. 27, Created)
DT 29-MAR-2004 (TREMblrel. 27, Last sequence update)
DT 29-MAR-2004 (TREMblrel. 27, Last annotation update)
DE Interleukin-6 (Fragment).
OS Cervus elaphus (Red deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae;
OC Cervinae; Cervus.
OX NCBI_TaxID=9860;
RN [1]
RP SEQUENCE FROM N.A.
RA O'Brien R., Berger S., Griffin F.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY540191; AAS73282.1; -.
FT NON TER 1 191

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FT NON TER 191 191
SQ SEQUENCE 191 AA; 21677 MW; 5936607DB4D3C1A0 CRC64;

Query Match 16.9%; Score 482.5; DB 2; Length 191;
Best Local Similarity 49.7%; Pred. No. 4.6e-26;
Matches 95; Conservative 40; Mismatches 49; Indels 7; Gaps 3;

QY 349 ANATSLVEFMPVPEDSKVAAPHROPLTSSERIDKQIRYLIDGIALRKETCKNSNM 408
DB 8 AMASAPFT---PGLGEDPKNDTPPSRLITTPKTEALIKHIVDKISARKKEICEKNDK 64
QY 409 CESSKEALANNINLPMKAEKDCGFCGSGFNETCLVKIITGLIEFEVYLEYLNRFSSSE 468
DB 65 CENSKETLAENNINLPMKKEKDCGFCGSGFNETCLIRSTVGLLEYQTYLDYLNQNEYEGDQ 124
QY 469 EQRNAVQMSKTVLIQLOKAKKRLDATTPTPTNASLITLQAOQNOIMQDMTHILRS 528
DB 125 ENVKDLRSSIRTLQIMRQ--KSIDLVT--ATTNPDLERKQSSNEWVKNAKIILIRS 180
QY 529 FKEFLQSSLR 539
DB 181 LENFLQPSLR 191

RESULT 31
IL6_CAPHI STANDARD; PRT; 208 AA.
ID IL6_CAPHI
AC Q28319;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interleukin-6 precursor (IL-6).
GN Name=IL6;
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Caprinae; Capra.
OX NCBI_TaxID=9925;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97392354; PubMed=9250586;
RA Takakura H., Mori Y., Tatsumi M.;
RT "Molecular cloning of caprine IL-6 cDNA and its expression in insect
cells.";
RL Int. Arch. Allergy Immunol. 113:409-416 (1997).
CC -1- FUNCTION: IL-6 is a cytokine with a wide variety of biological
functions: it plays an essential role in the final differentiation
of B-cells into Ig-secreting cells, it induces myeloma and
plasmacytoma growth, it induces nerve cells differentiation, in
hepatocytes it induces acute phase reactants.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the IL-6 superfamily.
CC -----
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CC -----
DR EMBL; D86569; BAA1318.1; -.
DR HS5P; P05231; IL6.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR InterPro; IPR003574; Interleukin_6.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR PRINTS; PR00434; INTERLEUKIN6.
DR PRODOM; PD004356; Interleukin_6; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
DR Acute phase; Cytokine; Glycoprotein; Growth factor; Signal.
KW

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FT SIGNAL 1 29 By similarity.
FT CHAIN 30 208 Interleukin-6.
FT DISULFID 72 78 By similarity.
FT DISULFID 101 111 By similarity.
FT CARBOHYD 38 38 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 208 AA; 23423 MW; E92E08BF3E3230A0 CRC64;

Query Match 16.5%; Score 472; DB 1; Length 208;
Best Local Similarity 51.1%; Pred. No. 2,9e-25;
Matches 93; Conservative 34; Mismatches 51; Indels 4; Gaps 2;

QY 360 PVPPEGDSKDVAAPHROPTSSERIDKQIRYILDGISALRKETCNKSNCESSKEALAEN 419
DB PGLGEDFNDPTPSRLITLTPKTEALIKRIVDKISARKKEICENKDECESSKETLAEN 88
QY 420 NNLTPMAEKDCGFGSGFNEETLVKIIITGLLEFEVYLEYLQNRPFSSSEQARAVQMSRK 479
DB KKLPRMEERKDCGFGSGFNOALCLRTTAGLLEYQIYLDYLFQNEFGNDETVNELQSSIR 148
QY 480 VLIQFLQKAKNLDATITPDPTTNASILTKLQAKONQWLODMTHLILRSFKEFLQSSLR 539
DB 149 TLIQILKEKAGL--ITT--PATNTMLEKMOSSNEWKNAKVIITLRLENFLQPSLR 204
QY 540 LR 541
DB 205 IR 206

RESULT 32
IL6_BOVIN STANDARD; PRT; 208 AA.
AC P26B92;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interleukin-6 precursor (IL-6).
GN Name=IL6;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OC NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Holstein;
RA MEDLINE=93076003; PubMed=1446077;
RA Drogmans L., Cludts I., Cleuter Y., Kettmann R., Burny A.;
RA "Nucleotide sequence of bovine interleukin-6 cDNA.";
RL DNA Seq. 2:411-413(1992).
CC -1- FUNCTION: IL-6 is a cytokine with a wide variety of biological
CC functions: it plays an essential role in the final differentiation
CC of B-cells into Ig-secreting cells. It induces myeloma and
CC plasmacytoma growth. It induces nerve cells differentiation, in
CC hepatocytes it induces acute phase reactants.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the IL-6 superfamily.
CC
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CC
CC EMBL; X57317; CAA40572.1; -.
CC PIR; A56610; A56610.
CC HSSP; POS231; IL6.
CC InterPro; IPR009079; 4 helix cytokine.
CC InterPro; IPR003573; IL6_MGF_GCSF.
CC InterPro; IPR003574; Interleukin_6.
CC Pfam; PF00489; IL6; 1.
CC PRINTS; PR00433; IL6GCSFMGF.

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DR PRINTS; PR00434; INTERLEUKIN6.
DR ProDom; PD004356; Interleukin_6; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
KW Acute phase; Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 29 By similarity.
FT CHAIN 30 208 Interleukin-6.
FT DISULFID 72 78 By similarity.
FT DISULFID 101 111 By similarity.
FT CARBOHYD 38 38 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 208 AA; 23758 MW; A0F00B9BA2EC341 CRC64;

Query Match 16.5%; Score 471; DB 1; Length 208;
Best Local Similarity 51.6%; Pred. No. 3,4e-25;
Matches 94; Conservative 33; Mismatches 51; Indels 4; Gaps 2;

QY 360 PVPPEGDSKDVAAPHROPTSSERIDKQIRYILDGISALRKETCNKSNCESSKEALAEN 419
DB PGLGEDFNDPTPGILLITPTEKTEALIKRWVDKISARKKEICENKDECESSKETLAEN 88
QY 420 NNLTPMAEKDCGFGSGFNEETLVKIIITGLLEFEVYLEYLQNRPFSSSEQARAVQMSRK 479
DB KNLPRMEERKDCGFGSGFNOALCLRTTAGLLEYQIYLDYLFQNEFGNDEVRDLKNIIR 148
QY 480 VLIQFLQKAKNLDATITPDPTTNASILTKLQAKONQWLODMTHLILRSFKEFLQSSLR 539
DB 149 TLIQIL--KQKTADLITT--PATNTDLEKMOSSNEWKNAKVIITLRLENFLQPSLR 204
QY 540 LR 541
DB 205 IR 206

RESULT 33
IL6_SHEEP STANDARD; PRT; 208 AA.
AC P29455;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interleukin-6 precursor (IL-6).
GN Name=IL6;
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Caprinae; Ovis.
OC NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=94041419; PubMed=8225400;
RA Andrews A.E., Barcham G.J., Ashman K., Meusen E.N.T., Brandon M.R.,
RA Nash A.D.;
RA "Molecular cloning and characterization of a ruminant interleukin-6
RT cDNA.";
RL Immunol. Cell Biol. 71:341-348(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC Submitted (OCT-1992) to the EMBL/GenBank/DBJ databases.
RL
CC -1- FUNCTION: IL-6 is a cytokine with a wide variety of biological
CC functions: it plays an essential role in the final differentiation
CC of B-cells into Ig-secreting cells. It induces myeloma and
CC plasmacytoma growth. It induces nerve cells differentiation, in
CC hepatocytes it induces acute phase reactants (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the IL-6 superfamily.
CC
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CC -----
 CC EMBL; X62501; CAA44363.1; -
 DR EMBL; X68723; CAA48662.1; -
 DR EMBL; A18159; CAA01443.1; -
 DR PIR; S29549; S29549.
 DR HSP; P05231; IL6.
 DR InterPro; IPR009079; 4_helix_cytokine.
 DR InterPro; IPR003573; IL6_MGF_GCSF.
 DR InterPro; IPR003574; Interleukin_6.
 DR Pfam; PF00489; IL6; 1.
 DR PRINTS; PR00433; IL6GCSFMGF.
 DR PRINTS; PR00434; INTERLEUKIN6.
 DR PRODOM; P0004356; Interleukin_6; 1.
 DR SMART; SM00126; IL6; 1.
 DR PROSITE; P500254; INTERLEUKIN_6; 1.
 DR Acute phase; Cytokine; Glycoprotein; Growth factor; Signal.
 KW SIGNAL 1 29
 FT CHAIN 1 29
 FT DISULFID 30 208
 FT DISULFID 72 78
 FT DISULFID 101 111
 FT CARBOHYD 38 38
 FT CONFLICT 4 4
 FT CONFLICT 110 110
 FT CONFLICT 171 171
 FT CONFLICT 201 201
 SQ SEQUENCE 208 AA; 23446 MW; EEC996C1B3320A0 CRC64;

Query Match 16.3%; Score 467; DB 1; Length 208;
 Best Local Similarity 50.5%; Pred. No. 6.4e-25;
 Matches 92; Conservative 35; Mismatches 51; Indels 4; Gaps 2;
 QY 360 PVPPEGDSKVAAAPHROPLTSSERIDKQIRYILDGISAARKETCNKSNMCCSSKEALAE 419
 DB 29 PGPLGDFPNDDTPGRLLTTPKTEBALIKRWVDKISARKETCNKSNMCCSSKEALAE 88
 QY 420 NLNLPKAEKDCGQSGFNEETCLVKITGLLEFEVYLEYLQNFESSEGOARAVOMSTK 479
 DB 89 KNLKPKAEKDCGQSGFNOAICLIRTAGLEVOYIYDLYQNEGNREVRDLKNTIR 148
 QY 480 VLIQFLQKAKNLDATTPPTTNASLITKLOQONQWLODMTHLILRSFKEFLOSIRA 539
 DB 149 TLIQIL--KQKADLIT--PATNTDLERKQSSNEWNAKATILILRNLENFLOFSIRA 204
 QY 540 LR 541
 DB 205 IR 206

RESULT 34
 ID 06V919 PRELIMINARY; PRT; 208 AA.
 AC QCV919;
 DT 05-JUL-2004 (Tremblrel. 27, Created)
 DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
 DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
 DE Interleukin 6.
 OS Bubalus bubalis (Domestic water buffalo).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bubalus.
 OC NCBI_TaxID=89462;
 OX NCBI [1]
 RN SEQUENCE FROM N.A.
 RP Premraj A., Sreekumar E., Rasool T.J.;
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY347710; AA054301.1; -
 DR InterPro; IPR009079; 4_helix_cytokine.
 DR InterPro; IPR003573; IL6_MGF_GCSF.
 DR InterPro; IPR003574; Interleukin_6.
 DR Pfam; PF00489; IL6; 1.
 DR PRINTS; PR00433; IL6GCSFMGF.
 DR PRINTS; PR00434; INTERLEUKIN6.

DR PRODOM; P0004356; Interleukin_6; 1.
 DR SMART; SM00126; IL6; 1.
 DR PROSITE; P500254; INTERLEUKIN_6; 1.
 DR SEQUENCE 208 AA; 23772 MW; 0C3F0374C52E7342 CRC64;

Query Match 16.3%; Score 466; DB 2; Length 208;
 Best Local Similarity 51.1%; Pred. No. 7.6e-25;
 Matches 93; Conservative 33; Mismatches 52; Indels 4; Gaps 2;
 QY 360 PVPPEGDSKVAAAPHROPLTSSERIDKQIRYILDGISAARKETCNKSNMCCSSKEALAE 419
 DB 29 PGPLGDFPNDDTPGRLLTTPKTEBALIKRWVDKISARKETCNKSNMCCSSKEALAE 88
 QY 420 NLNLPKAEKDCGQSGFNEETCLVKITGLLEFEVYLEYLQNFESSEGOARAVOMSTK 479
 DB 89 KNLKPKAEKDCGQSGFNOAICLIRTAGLEVOYIYDLYQNEGNREVRDLKNTIR 148
 QY 480 VLIQFLQKAKNLDATTPPTTNASLITKLOQONQWLODMTHLILRSFKEFLOSIRA 539
 DB 149 TLIQIL--KQKADLIT--PATNTDLERKQSSNEWNAKATILILRNLENFLOFSIRA 204
 QY 540 LR 541
 DB 205 IR 206

RESULT 35
 ID AA054301 PRELIMINARY; PRT; 208 AA.
 AC AA054301;
 DT 02-MAR-2004 (Tremblrel. 27, Created)
 DT 02-MAR-2004 (Tremblrel. 27, Last sequence update)
 DT 02-MAR-2004 (Tremblrel. 27, Last annotation update)
 DE Interleukin 6.
 OS Bubalus bubalis (Domestic water buffalo).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bubalus.
 OC NCBI_TaxID=89462;
 RN [1]
 RP Premraj A., Sreekumar E., Rasool T.J.;
 RA "Identification and molecular characterization of major Th2 cytokines
 of Indian water buffalo (Bubalus bubalis)."
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY347710; AA054301.1; -
 DR SEQUENCE 208 AA; 23772 MW; 0C3F0374C52E7342 CRC64;

Query Match 16.3%; Score 466; DB 2; Length 208;
 Best Local Similarity 51.1%; Pred. No. 7.6e-25;
 Matches 93; Conservative 33; Mismatches 52; Indels 4; Gaps 2;

QY 360 PVPPEGDSKVAAAPHROPLTSSERIDKQIRYILDGISAARKETCNKSNMCCSSKEALAE 419
 DB 29 PGPLGDFPNDDTPGRLLTTPKTEBALIKRWVDKISARKETCNKSNMCCSSKEALAE 88
 QY 420 NLNLPKAEKDCGQSGFNEETCLVKITGLLEFEVYLEYLQNFESSEGOARAVOMSTK 479
 DB 89 KNLKPKAEKDCGQSGFNOAICLIRTAGLEVOYIYDLYQNEGNREVRDLKNTIR 148
 QY 480 VLIQFLQKAKNLDATTPPTTNASLITKLOQONQWLODMTHLILRSFKEFLOSIRA 539
 DB 149 TLIQIL--KQKADLIT--PATNTDLERKQSSNEWNAKATILILRNLENFLOFSIRA 204

RESULT 36
 ID IL6_MARMO STANDARD; PRT; 207 AA.
 AC 035736;


```

DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interleukin-6 precursor (IL-6).
GN Name=IL6;
OS Marmota monax (Woodchuck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Scuridae; Sciurinae;
OC Marmota.
NCBI_TaxID=9995;
RN NCBITaxID=9995;
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral blood;
RX MEDLINE=98139533; PubMed=9472070;
RA Lohengr B., Lu M., Rogendorf M.;
RT "Molecular cloning of the woodchuck cytokines: TNF-alpha, IFN-gamma,
RT and IL-6."
RL Immunogenetics 47:332-335(1998).
CC -1- FUNCTION: IL-6 is a cytokine with a wide variety of biological
CC functions: it plays an essential role in the final differentiation
CC of B-cells into Ig-secreting cells, it induces myeloma and
CC plasmacytoma growth, it induces nerve cells differentiation, in
CC hepatocytes it induces acute phase reactants (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the IL-6 superfamily.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Y14139; CAA74571.1; -.
DR HSSP; P05231; 1ALU.
DR InterPro; IPR009079; 4 helix cytokine.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR InterPro; IPR003574; Interleukin_6.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR PRINTS; PR00434; INTERLEUKIN6.
DR ProDom; PD004356; Interleukin_6; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
KW Acute phase; Cytokine; Glycoprotein; Growth factor; Signal.
FT CHAIN 1 18 Potential.
FT DISULFID 19 207 Interleukin-6.
FT DISULFID 65 71 By similarity.
FT DISULFID 94 104 By similarity.
SQ SEQUENCE 207 AA; 23770 MW; F30D19F86AD6A600 CRC64;
Query Match 15.3%; Score 437.5; DB 1; Length 207;
Best Local Similarity 45.4%; Pred. No. 7,7e-23;
Matches 88; Conservative 39; Mismatches 62; Indels 5; Gaps 2;
QY 351 ATSLPVEFMPVPPGDSKVAAAPHRQPLTSSEIRIDKQIRYILGIGSLARKETCNKSMCE 410
DB 16 ATAFPASELQREDGENSVTRNKPTR--ASSGKTRRQISYLIREVEMRKELKNDCTCI 72
QY 411 SSKKALAEENLNLPKAAEKDQCFQSGFNEETCLVKITITGLLEFVLYEYVLYONPESSEEQ 470
DB 73 KSHVAVSENNLTNPKTEKDCGCFQGYVNDNCVLRITSGLEFQVLYRYIRNKFQSGNNR 132
QY 471 ARA--VQMGSTKVLIOFLQKAKNLDAITPDPPTNASLTKLQAQONQWLODMTHILRS 528
DB 133 DRAEHVQSSSKALIEILKQEVKDPNKIVPSPPTANINILAKESQNDQWQVMQMOLILSN 192
QY 529 KFEFLQSSSLRALRQ 542
DB 193 FEDFLQFTLRVRK 206

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RESULT 37
Q9JHH3 PRELIMINARY; PRT; 207 AA.
AC Q9JHH3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Interleukin-6.
GN Name=IL-6;
OS Marmota monax (Woodchuck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Scuridae; Sciurinae;
OC Marmota.
NCBI_TaxID=9995;
RN NCBITaxID=9995;
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral blood;
RA Li D.H., Cullen U.M.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Li D.H., Cullen U.M.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RX MEDLINE=21536769; PubMed=11679978;
RA Hodgson P.D., Michalak T.I.;
RT "Augmented hepatic interferon gamma expression and T-cell influx
RT characterize acute hepatitis progressing to recovery and residual
RT lifelong virus persistence in experimental adult woodchuck hepatitis
RT virus infection."
RL Hepatology 34:1049-1059(2001).
DR EMBL; AF012808; AAF34861.1; -.
DR EMBL; AF12896; AAF28673.1; -.
DR EMBL; AF333966; AAK52717.1; -.
DR HSSP; P05231; 1ALU.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005125; F:cytokine activity; IEA.
DR GO; GO:0005138; F:interleukin-6 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR009079; 4 helix cytokine.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR InterPro; IPR003574; Interleukin_6.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR PRINTS; PR00434; INTERLEUKIN6.
DR ProDom; PD004356; Interleukin_6; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
SQ SEQUENCE 207 AA; 23645 MW; AD2F46E450E13470 CRC64;
Query Match 15.2%; Score 435.5; DB 2; Length 207;
Best Local Similarity 45.4%; Pred. No. 1.1e-22;
Matches 88; Conservative 38; Mismatches 63; Indels 5; Gaps 2;
QY 351 ATSLPVEFMPVPPGDSKVAAAPHRQPLTSSEIRIDKQIRYILGIGSLARKETCNKSMCE 410
DB 16 ATAFPASELQREDGENSVTRNKPTR--ASSGKTRRQISYLIREVEMRKELKNDCTCI 72
QY 411 SSKKALAEENLNLPKAAEKDQCFQSGFNEETCLVKITITGLLEFVLYEYVLYONPESSEEQ 470
DB 73 KSHVAVSENNLTNPKTEKDCGCFQGYVNDNCVLRITSGLEFQVLYRYIRNKFQSGNNR 132
QY 471 ARA--VQMGSTKVLIOFLQKAKNLDAITPDPPTNASLTKLQAQONQWLODMTHILRS 528
DB 133 DRAEHVQSSSKALIEILKQEVKDPNKIVPSPPTANINILAKESQNDQWQVMQMOLILSN 192
QY 529 KFEFLQSSSLRALRQ 542
DB 193 FEDFLQFTLRVRK 206

```

RESULT 38

CC or send an email to license@sb-slb.ch).

CC EMBL; M26744; AAA77659.1; -.
 DR EMBL; M26745; AAA1430.1; -.
 DR PIR; A34247; A34247.
 DR HSSP; P05231; IALU.
 DR RGD; 2901; IL6.
 DR InterPro; IPR009079; 4 helix cytokine.
 DR InterPro; IPR003573; IL6 MGF GCSE.
 DR InterPro; IPR003574; Interleukin_6.
 DR Pfam; PF00489; IL6; 1.
 DR PRINTS; PR00433; IL6GCFMGF.
 DR ProDom; PD004356; Interleukin_6; 1.
 DR SMART; SM00126; IL6; 1.
 DR PROSITE; PS00254; INTERLEUKIN_6; 1.
 KW Acute phase; Cytokine; Glycoprotein; Growth factor; Signal.
 FT SIGNAL 1 24 potential.
 FT CHAIN 25 211 Interleukin-6.
 FT DISULFID 70 76 By similarity.
 FT DISULFID 99 109 By similarity.
 SQ SEQUENCE 211 AA; 24357 MW; 17D248A14F96B5C1 CRC64;

Query Match 13.9%; Score 396.5; DB 1; Length 211;
 Best Local Similarity 39.4%; Pred. No. 6, 1e-20;
 Matches 76; Conservative 53; Mismatches 59; Indels 5; Gaps 3;

QY 351 ATSLPVEFMPVPPGDESKVVAAPHROPLTSSERIDKOIRIYLDGISALRKETCKNSMCE 410
 DB 22 ATAFPTS--QVRGDPTEDTT--HNRPVYTTSQVGGITVLRILEIMRKELCNGNSDCM 77
 QY 411 SSKBALAENNLLNPKMAEKDGFQSGPNEETCLVKIITGLPEFVYLVYQNR-ESSEE 469
 DB 78 NSDDALSENNLKLPEIQKNDGCFQTGYNOETCLKICGLLEFRFYLFYKNNLQDKKD 137
 QY 470 QARAVQSTKVLIQFLQKAKNLDAITPDPITNASLLTKLQANQMLQDMTHILRSF 529
 DB 138 KARVIGSNTEVLVHIFKQEKDSYKIVLPPTSNALLMEXLESQKEMLRKTIQLILKAL 197
 QY 530 KEFLQSSLRALRQ 542
 DB 198 EEFLKVTMRSTRQ 210

Search completed: December 9, 2004, 09:20:54
 Job time : 252.038 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 9, 2004, 08:55:07 ; Search time 1.14568 Seconds
(without alignments)
1091.766 Million cell updates/sec

Title: US-09-462-416-1

Perfect score: 67

Sequence: 1 EFGAGLVLCGCFM 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	68.7	382	2 AC3118	transcription regu
2	46	68.7	402	2 D98169	trcr protein (Afl19
3	46	68.7	1171	1 QOKBFP	pyruvate (flavodox
4	42	62.7	396	2 B75290	hypothetical prote
5	41	61.2	291	2 E71491	probable geranyl t
6	41	61.2	313	2 S66962	probable membrane
7	41	61.2	347	2 D83605	probable binding p
8	41	61.2	623	2 S56206	probable membrane
9	41	61.2	920	2 C70668	probable mmp17 pro
10	40	59.7	232	1 S28609	phosphadenylyl-su
11	40	59.7	492	2 A87471	hypothetical prote
12	40	59.7	579	2 B82085	sensory box/GGDEF
13	40	59.7	1617	2 B86483	protein F505.15 [1
14	39	58.2	220	2 E71857	probable outer mem
15	39	58.2	230	2 C64658	outer membrane pro
16	39	58.2	274	2 H72521	probable thiazole
17	39	58.2	308	2 H81685	conserved hypotet
18	39	58.2	632	2 B71326	probable V-type AT
19	39	58.2	770	2 S56805	probable RNA helic
20	38.5	57.5	880	2 F83386	hypothetical prote
21	38	56.7	127	2 A53952	profilin - fibron
22	38	56.7	147	2 AG3578	hypothetical prote
23	38	56.7	171	2 T11285	NADH dehydrogenas
24	38	56.7	249	2 T09139	26S proteasome alp
25	38	56.7	272	2 G84667	20S proteasome sub
26	38	56.7	272	2 A84747	ABC transporter, m
27	38	56.7	298	2 AD2715	probable Fe(II) tr
28	38	56.7	348	2 T06385	hypothetical prote
29	38	56.7	389	2 T28954	hypothetical prote

30	38	56.7	390	2 T40924	nuclear localizati
31	38	56.7	494	2 G97496	integral membrane
32	38	56.7	630	2 AB3463	hypothetical membr
33	38	56.7	748	2 G96498	hypothetical prote
34	38	56.7	754	2 AB0614	probable compen
35	38	56.7	1195	2 S76592	5-methyltetrahydro
36	37	55.2	61	2 D64012	hypothetical prote
37	37	55.2	150	2 JS0297	infection structur
38	37	55.2	181	2 AH1737	NADH-dependent FMN
39	37	55.2	233	2 A72786	probable transport
40	37	55.2	261	2 AE1471	hypothetical prote
41	37	55.2	303	2 A71529	hypothetical prote
42	37	55.2	352	2 S45558	cytochrome c-type
43	37	55.2	413	2 JC2520	beta-fructofuranos
44	37	55.2	416	2 D84638	probable sarcosine
45	37	55.2	418	2 H83316	isocitrate dehydro

ALIGNMENTS

RESULT 1
AC3118
transcription regulator, ROK family Atu4567 [imported] - Agrobacterium tumefaciens (stra)
C/Species: Agrobacterium tumefaciens
C/Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C/Accession: AC3118
R/Wood, D.W.; Sebald, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kuyavlin, T.; Levy, R.; Li, M.; McClellan
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, E
ster, E.W.
A/Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A/Reference number: AB2577; MUID:21608550; PMID:11743193
A/Accession: AC3118
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-382 <KUR>
A/Cross-references: UNIPROT:Q8U787; GB:AE008689; PIDN:ALL45361.1; PID:gl7743056; GSPDB:GT
A/Experimental source: strain C58 (Dupont)
C/Genetics:
A/Genes: Atu4567
A/Map position: linear chromosome
Query Match 68.7%; Score 46; DB 2; Length 382;
Best Local Similarity 80.0%; Pred. No. 3.6;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2 FEGAGLVLCG 11
DB 226 FEGAGLVLCG 235
RESULT 2
trcr protein (Afl196574) [imported] - Agrobacterium tumefaciens (strain C58, Cereon)
C/Species: Agrobacterium tumefaciens
C/Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C/Accession: D98169
R/Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorillo, B.; Goldman,
A.; Liu, F.; Molim, C.; Allinger, M.; Doughy, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A/Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tume
A/Reference number: A97359; MUID:21608551; PMID:11743194
A/Accession: D98169
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-402 <KUR>
A/Cross-references: UNIPROT:Q8U787; GB:AE007870; PIDN:AAK88878.1; PID:gl5158645; GSPDB:GT
C/Genetics:
A/Genes: AGR_L_609
A/Map position: linear chromosome

R.Bohn, C.; Bolotin-Fukuhara, M.; Daignan-Fornier, B.; Dang, D.V.; Valens, M.
submitted to the Protein Sequence Database, July 1996
A:Reference number: S66929
A:Accession: S66962
A:Molecule type: DNA
A:Residues: 1-313 <BOH>
A:Cross-references: UNIPROT:Q12067; EMBL:Z74987; NID:g1420238; PID:e251990; PID:g1420239
A:Experimental source: strain S286C
C:Genetics:
A:Gene: SGD:ATX2
A:Cross-references: SGD:S0005605; MIPS:YOR079C
A:Map position: 15R
C:Keywords: transmembrane protein
F:7-23/Domain: transmembrane #status predicted <TM1>
F:76-92/Domain: transmembrane #status predicted <TM2>
F:106-122/Domain: transmembrane #status predicted <TM3>
F:160-176/Domain: transmembrane #status predicted <TM4>
F:184-200/Domain: transmembrane #status predicted <TM5>
F:222-238/Domain: transmembrane #status predicted <TM6>
F:294-310/Domain: transmembrane #status predicted <TM7>

Query Match 61.2%; Score 41; DB 2; Length 313;
Best Local Similarity 53.8%; Pred. No. 21;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EFAGGLVIGGQFM 13
DB 73 QFELGMLGTSFM 85

RESULT 7
D83605
probable binding protein component of ABC transporter PA0323 [imported] - Pseudomonas aeruginosa
C:Species: Pseudomonas aeruginosa
C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C:Accession: D83605
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.D.; Adams, S.; Ryan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kae, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: D83605
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-347 <STO>
A:Cross-references: UNIPROT:Q916G8; GB:AE004470; GB:AE004091; NID:g9946164; PIDN:AA0371
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA0323
C:Superfamily: Escherichia coli spermidine/putrescine-binding protein

Query Match 61.2%; Score 41; DB 2; Length 347;
Best Local Similarity 80.0%; Pred. No. 23;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 FGAGLVIGGQ 11
DB 11 FAAGLALGGQ 20

RESULT 8
S56206
Probable membrane protein YFL049w - Yeast (Saccharomyces cerevisiae)
C:Species: Saccharomyces cerevisiae
C>Date: 02-Sep-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
C:Accession: S56206
R:Murkanti, Y.; Naitou, M.; Hagiwara, H.; Shibata, T.; Ozawa, M.; Sasanuma, S.I.; Sasano, M.
submitted to the EMBL Data Library, May 1995
A:Description: Analysis of the nucleotide sequence of chromosome VI from Saccharomyces cerevisiae
A:Reference number: S56186
A:Accession: S56206
A:Status: preliminary

A:Molecule type: DNA
A:Residues: 1-623 <MUR>
A:Cross-references: UNIPROT:P43554; EMBL:D50617; NID:g836685; PID:d1009830; PID:g836706;
C:Genetics:
A:Cross-references: SGD:S0001845
A:Map position: 6L
C:Keywords: transmembrane protein
F:121-137/Domain: transmembrane #status predicted <TM1>

Query Match 61.2%; Score 41; DB 2; Length 623;
Best Local Similarity 63.6%; Pred. No. 40;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 EFAGGLVIGGQ 11
DB 194 EFAGSVIAGGQ 204

RESULT 9
C70668
probable mmpL7 protein - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C:Accession: C70668
R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Rajandream, M.A.; Rogers, J.; Devlin, K.; Felwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Nature 393, 537-544, 1998
A:Authors: Squires, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: C70668
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-920 <COL>
A:Cross-references: UNIPROT:P96289; GB:Z83858; GB:AL123456; NID:g3261675; PIDN:CAB06107.1
A:Experimental source: strain H37RV
C:Genetics:
A:Gene: mmpL7

Query Match 61.2%; Score 41; DB 2; Length 920;
Best Local Similarity 76.9%; Pred. No. 59;
Matches 10; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

QY 2 FGAGLVIGGQ 12
DB 876 FGAGLVISGSF 888

RESULT 10
S28609
phosphoadenylyl-sulfate reductase (thioredoxin) (EC 1.8.4.8) - Synechococcus sp. (strain N:containing 3'-phosphoadenylylsulfate reductase, thioredoxin dependent; PAPS reduced; C:Species: Synechococcus sp.
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: S28609
R:Nienhaus, A.; Gisselmann, G.; Schwenn, J.D.
Plant Mol. Biol. 20, 1179-1183, 1992
A:Title: Primary structure of the Synechococcus PCC 7942 PAPS reductase gene.
A:Reference number: S28609; MUID:9309269; PMID:1463852
A:Accession: S28609
A:Molecule type: DNA
A:Residues: 1-232 <NIE>
A:Cross-references: UNIPROT:O55309; EMBL:M84476; NID:g154543; PIDN:AAA27328.1; PID:g15454
C:Genetics:
A:Gene: par
C:Superfamily: 3'-phosphoadenosine 5'-phosphosulfate reductase
C:Keywords: cysteine biosynthesis; oxidoreductase; sulfotransferase

Query Match 59.7%; Score 40; DB 1; Length 232;
Best Local Similarity 66.7%; Pred. No. 23;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EFAGLVLGGQF 12
 |||:||||
 Db 30 EFSGGLVLSRF 41

RESULT 11
 A:7471
 hypothetical protein CCI789 [imported] - Caulobacter crescentus
 C:Species: Caulobacter crescentus
 C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
 C:Accession: A87471
 R:Nernan, W.C.; Feldblum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
 B.; Laub, M.T.; Deboy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
 n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
 Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
 A:Title: Complete Genome Sequence of Caulobacter crescentus.
 A:Reference number: A87499; MUID:21173698; PMID:11259647
 A:Accession: A87471
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-492 <STO>
 A:Cross-references: UNIPROT:Q9A7D4; GB:AE005673; NID:913423219; PIDN:AAK23765.1; GSPDB:G
 C:Genetics:
 A:Gene: CCI789

Query Match 59.7%; Score 40; DB 2; Length 492;
 Best Local Similarity 77.8%; Pred. No. 48;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 FGAGLVGG 10
 |||||:|
 Db 93 FGAGLVGG 101

RESULT 12
 B82085
 sensory box/GDEF family protein VC2370 [imported] - Vibrio cholerae (strain N16961 serc
 C:Species: Vibrio cholerae
 C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
 C:Accession: B82085
 R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
 charidson, D.; Ermolaeva, M.D.; Vamthekavan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, F
 l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
 Nature 406, 447-483, 2000
 A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
 A:Reference number: A82035; MUID:20406833; PMID:10952301
 A:Accession: B82085
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-579 <HEI>
 A:Cross-references: UNIPROT:Q9KRJ7; GB:AE004307; GB:AE003852; NID:93656934; PIDN:AAF9551
 A:Experimental source: serogroup O1; strain N16961; biotype El Tor
 C:Genetics:
 A:Gene: VC2370
 A:Map position: 1

Query Match 59.7%; Score 40; DB 2; Length 579;
 Best Local Similarity 88.9%; Pred. No. 56;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 FGAGLVGG 10
 |||||:|
 Db 13 FGAGLVGG 21

RESULT 13
 B86483
 protein FSU5.15 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C:Accession: B86483
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
 ansen, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; MUID:21016719; PMID:11130712
 A:Accession: B86483
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1617 <STO>
 A:Cross-references: UNIPROT:Q9SKV5; GB:AE005172; NID:96598587; PIDN:AAF18642.1; GSPDB:GNC
 C:Genetics:
 A:Gene: FSU5.15
 A:Map position: 1

Query Match 59.7%; Score 40; DB 2; Length 1617;
 Best Local Similarity 53.8%; Pred. No. 1.5e+02;
 Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EFAGLVLGGQFM 13
 |||||:|
 Db 458 OFGAVKXGGQFL 470

RESULT 14
 E71857
 probable outer membrane protein - Helicobacter pylori (strain J99)
 C:Species: Helicobacter pylori
 A:Variety: strain J99
 C>Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
 C:Accession: E71857
 R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
 Ives, C.; Gibson, R.; Webberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; J
 Nature 397, 176-180, 1999
 A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
 A:Reference number: A71800; MUID:99120557; PMID:9923682
 A:Accession: E71857
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-220 <ARN>
 A:Cross-references: UNIPROT:Q9ZKA5; GB:AE001531; GB:AE001439; NID:94155617; PIDN:AAD0661;
 A:Experimental source: strain J99
 C:Genetics:
 A:Gene: jhp1034

Query Match 58.2%; Score 39; DB 2; Length 220;
 Best Local Similarity 63.6%; Pred. No. 33;
 Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 GAGVLVGGQFM 13
 |||||:|
 Db 70 GFGVLGGKRV 80

RESULT 15
 C64658
 outer membrane protein - Helicobacter pylori (strain 26695)
 C:Species: Helicobacter pylori
 C>Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
 C:Accession: C64658
 R:Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.;
 Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalaf, H.G.; Glodek, A.; McKenney
 son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.
 Nature 388, 539-547, 1997
 A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karp, P.D.; Smith, H.O.; Fraser, C.A
 A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
 A:Reference number: A64520; MUID:97394467; PMID:9252185
 A:Accession: C64658
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA
A:Residues: 1-230 <TOM>
A:Cross-references: UNIPROT:O25735; GB:AE000617; GB:AE000511; NID:92314256; PIDN:AAD0816
C:Genetics:
A:Start codon: GTG

Query Match 58.2%; Score 39; DB 2; Length 230;
Best Local Similarity 63.6%; Pred. No. 34;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 GAGLVGQGM 13
|:|:|:|:|:
DB 80 GEGVLGGRFV 90

RESULT 16
H7521
probable thiazole biosynthetic enzyme ABE2149 - Aeropyrum pernix (strain K1)

C:Species: Aeropyrum pernix
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C:Accession: H7521

R:Kawabuchi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahawa, H.; Takamiya, M.; Maeda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; KDNA Res. 6, 83-101, 1999
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrum

A:Reference number: A72450; NID:99310339; PMID:10382966

A:Accession: H7521
A:Status: preliminary

A:Molecule type: DNA
A:Residues: 1-274 <RAW>

A:Cross-references: UNIPROT:Q9Y9Z0; DDBJ:AP000063; NID:95105654; PIDN:BAA81160.1; PID:95
C:Genetics:
A:Gene: ABE2149

C:Superfamily: thiamin biosynthesis protein th1

Query Match 58.2%; Score 39; DB 2; Length 274;
Best Local Similarity 72.7%; Pred. No. 40;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GAGLVGQGM 13
|:|:|:|:|:
DB 68 GGGVLGGRFV 78

RESULT 17

H81685
conserved hypothetical protein TC0598 [imported] - Chlamydia muridarum (strain N195)

C:Species: Chlamydia muridarum, Chlamydia trachomatis Mohn
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C:Accession: H81685

R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodeon, R.; Gilm, M.; Nelson, W.; Deboy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000
A:Title: Genome sequences of Chlamydia trachomatis Mohn and Chlamydia pneumoniae A39.

A:Reference number: A81500; NID:20150255; PMID:10684935

A:Accession: H81685
A:Status: preliminary

A:Molecule type: DNA
A:Residues: 1-308 <TET>

A:Cross-references: UNIPROT:Q9PK72; GB:AE002328; GB:AE002160; NID:9710627; PIDN:AAF3943
A:Experimental source: strain N195 (Mohn)

C:Genetics:
A:Gene: TC0598

Query Match 58.2%; Score 39; DB 2; Length 308;
Best Local Similarity 87.5%; Pred. No. 45;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 FGAGLVG 9
|:|:|:|:|:
DB 105 FGAGLVG 112

RESULT 18

B71326
probable V-type ATPase, subunit I (atp1-1) - Syphilis spirochete

C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C:Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C:Accession: B71326

R:Praser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDerby, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998

A:Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A:Reference number: A71250; NID:98332770; PMID:9665876

A:Accession: B71326
A:Status: preliminary

A:Molecule type: DNA
A:Residues: 1-622 <COL>

A:Cross-references: UNIPROT:O83444; GB:AE001220; GB:AE000520; NID:93322705; PIDN:AA66541;
A:Experimental source: strain Nichols

C:Genetics:
A:Gene: TP0429

Query Match 58.2%; Score 39; DB 2; Length 622;
Best Local Similarity 53.8%; Pred. No. 88;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 EFGAGLVGQGM 13
|:|:|:|:|:
DB 460 EFGSLMLGGMV 472

RESULT 19

S56805
probable RNA helicase CA4 - yeast (Saccharomyces cerevisiae)

N:Alternate names: protein YJ1250; protein YJL033w
C:Species: Saccharomyces cerevisiae
C:Date: 08-Jul-1995 #sequence_revision 08-Sep-1995 #text_change 09-Jul-2004
C:Accession: S56805; C34848

R:Polh, T.M.; Aljinovic, G.
submitted to the Protein Sequence Database, September 1995

A:Reference number: S56793
A:Accession: S56805

A:Molecule type: DNA
A:Residues: 1-770 <TOV>

A:Cross-references: UNIPROT:P20448; EMBL:Z49308; NID:91008154; PIDN:CAA89324.1; PID:91008

R:Chang, T.H.; Arenas, J.; Abelson, J.
Proc. Natl. Acad. Sci. U.S.A. 87, 1571-1575, 1990

A:Title: Identification of five putative yeast RNA helicase genes.
A:Reference number: A34848; NID:90160368; PMID:2406722

A:Accession: C34848
A:Molecule type: DNA

A:Residues: 192-380, 'I', 382 <CHA>

C:Genetics:
A:Gene: SGD:HCA4

A:Cross-references: SGD:S0003570; MIPS:YJL033w
A:Map position: 10L

C:Keywords: ATP; nucleotide binding; P-loop
F:85-92/Region: nucleotide-binding motif A (P-loop)
F:190-195/Region: nucleotide-binding motif B

F:194-197/Region: DEAD motif

Query Match 58.2%; Score 39; DB 2; Length 770;
Best Local Similarity 70.0%; Pred. No. 11e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 FGAGLVGQ 11
|:|:|:|:|:
DB 142 FSGAGLVGK 151

RESULT 20

F83386
hypothetical protein PA2070 [imported] - Pseudomonas aeruginosa (strain PA01)

A:Reference number: Z16562; MUID:97351564; PMID:9207846
A:Accession: T09139
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-249 <1TO>
A:Cross-references: UNIPROT:Q24362; EMBL:D78173; NID:G2285801; PIDN:BA21651.1; PID:G228
C:Superfamily: multicatalytic endopeptidase complex chain C9

Query Match 56.7%; Score 38; DB 2; Length 249;
Best Local Similarity 66.7%; Pred. No. 54;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 FGAGLVGG 10
DB 132 FCGGVILGG 140

RESULT 25
G84667
20S proteasome subunit C8 (PAG1/PRC8 ARATH) [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: G84667
R:Lin, X.; Kaul, S.; Rounbley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Venkatesh, S.E.; Umayam, L.; Tallon, L.;
Euse, D.; Niernan, W.C.; White, O.; Eisen, J.A.; Salberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A>Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: G84667
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-249 <STO>
A:Cross-references: UNIPROT:Q23715; GB:AE002093; NID:G3885332; PIDN:AACT7860.1; GSPDB:GN
C:Genetics:
A:Gene: Atg27020
A:Map position: 2
C:Superfamily: multicatalytic endopeptidase complex chain C9

Query Match 56.7%; Score 38; DB 2; Length 249;
Best Local Similarity 66.7%; Pred. No. 54;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 FGAGLVGG 10
DB 132 FCGGVILGG 140

RESULT 26
A84747
hypothetical protein At2g33560 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: A84747
R:Lin, X.; Kaul, S.; Rounbley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Venkatesh, S.E.; Umayam, L.; Tallon, L.;
Euse, D.; Niernan, W.C.; White, O.; Eisen, J.A.; Salberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A>Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: A84747
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-272 <STO>
A:Cross-references: UNIPROT:Q22806; GB:AE002093; NID:G2459438; PIDN:AA80673.1; GSPDB:GN
C:Genetics:
A:Gene: At2g33560
A:Map position: 2

Query Match 56.7%; Score 38; DB 2; Length 272;
Best Local Similarity 63.6%; Pred. No. 59;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EFGAGLVGG 11
DB 215 EFGSWLMGGR 225

RESULT 27
AD2715
ABC transporter, membrane spanning protein Atu1125 [imported] - Agrobacterium tumefaciens
C:Species: Agrobacterium tumefaciens
C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C:Accession: AD2715
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.;
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kuyavin, T.; Levy, R.; Li, M.; McClellan,
Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, I.
ster, E.W.
A>Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: AD2715
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-258 <KUR>
A:Cross-references: UNIPROT:Q8UGB3; GB:AE008688; PIDN:AA42138.1; PID:G17739523; GSPDB:GT
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: Atu1125
A:Map position: circular chromosome

Query Match 56.7%; Score 38; DB 2; Length 298;
Best Local Similarity 77.8%; Pred. No. 64;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EFGAGLVGG 9
DB 227 EFGAGLVGG 235

RESULT 28
T06385
probable Fe(II) transport protein, root - garden pea
C:Species: Pisum sativum (garden pea)
C>Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004
C:Accession: T06385
R:Cohen, C.K.; Fox, T.C.; Garvin, D.F.; Kochian, L.V.
Plant Physiol. 116, 1063-1072, 1998
A>Title: The role of iron-deficiency stress responses in stimulating heavy-metal transpo
A:Reference number: Z15642
A:Accession: T06385
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-348 <COH>
A:Cross-references: UNIPROT:Q65348; EMBL:AF065444; NID:G3153888; PIDN:AACT7441.1; PID:G33
A:Experimental source: cultivar Sparkle
C:Genetics:
A:Gene: Rict1
C:Superfamily: Arabidopsis thaliana zinc transporter ZIP1

Query Match 56.7%; Score 38; DB 2; Length 348;
Best Local Similarity 58.3%; Pred. No. 74;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 FGAGLVGGQFM 13
DB 87 FAAGIILGTFM 98

RESULT 29
T28954
hypothetical protein F28A12.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T28954

us-09-462-416-1.rpt

Fri Dec 10 08:14:22 2004

R.Sammons, L.; Murray, J.
submitted to the EMBL Data Library, July 1996

A:Description: The sequence of C. elegans cosmid F28A12.

A:Reference number: Z20547

A:Accession: F28954

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-389 <SMM>

A:Cross-references: UNIPROT:Q22972; EMBL:U54851; PIDN:AA47989.1; GSPDB:GN00023; CESP:F2

A:Experimental source: strain Bristol N2; clone F28A12

C:Genetics:

A:Gene: CESP:F28A12.4

A:Map position: 5

A:Introns: 104/2; 147/3; 175/3; 258/3; 301/3; 341/3

C:Superfamily: pepsin

Query Match

Best Local Similarity

Matches

QY

DB

1 EFAGLVGQFM 13

357 FGPSWILGQFPM 368

56.7%; Score 38; DB 2; Length 389;

77.8%; Pred. No. 83;

1; Mismatches

4; Indels

0; Gaps

0; Indels

0; Gaps

0; Indels

0; Gaps

0; Indels

0; Gaps

0; Indels

0; Gaps

0; Indels

0; Gaps

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0; Indels

0; Gaps

0; Indels

0; Gaps

0; Indels

0; Gaps

0; Indels

0; Gaps

0; Indels

Query Match

Best Local Similarity

Matches

QY

DB

1 EFAGLVGQ 9

423 DFAGLVGQ 431

56.7%; Score 38; DB 2; Length 494;

77.8%; Pred. No. 16+02; 1; Indels

1; Mismatches

0; Gaps

0; Indels

0; Gaps

0; Indels

0; Gaps

0; Indels

0; Gaps

0; Indels

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0; Gaps

0; Indels

0; Gaps

0; Indels

0; Gaps

0; Indels

0; Gaps

Query Match

Best Local Similarity

Matches

QY

DB

1 EFAGLVGQFM 13

265 QFGSVKAVAGQFL 277

56.7%; Score 38; DB 2; Length 748;

77.8%; Pred. No. 1.5e+02; 3; Indels

3; Mismatches

0; Gaps

0; Indels

0; Gaps

0; Indels

0; Gaps

0; Indels

0; Gaps

0; Indels

0; Gaps

0; Indels

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0; Gaps

Query Match

Best Local Similarity

Matches

QY

DB

1 EFAGLVGQFM 13

265 QFGSVKAVAGQFL 277

56.7%; Score 38; DB 2; Length 748;

77.8%; Pred. No. 1.5e+02; 3; Indels

3; Mismatches

0; Gaps

0; Indels

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0; Indels

0; Gaps

Query Match

Best Local Similarity

Matches

QY

DB

1 EFAGLVGQFM 13

265 QFGSVKAVAGQFL 277

56.7%; Score 38; DB 2; Length 748;

77.8%; Pred. No. 1.5e+02; 3; Indels

3; Mismatches

0; Gaps

0; Indels

0; Gaps

0; Indels

0; Gaps

0; Indels

0; Gaps</

RESULT 34
AE0614
probable competence-related protein STY0984 [imported] - *Salmonella enterica* subsp. *enterica*
C:Species: *Salmonella enterica* subsp. *enterica* serovar Typhimurium
A:Note: this species has also been called *Salmonella typhi*
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 25-Aug-2003
C:Accession: AE0614
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, M.; T. Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Garra, P.
Nucleotide 413, 848-852, 2001
A:Authors: Park, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.
A:Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serovar Typhimurium
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AE0614
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-754 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD05383.1; PID:gl6502146; GSPDB:GN00176
C:Genetics:
A:Gene: STY0984
C:Superfamily: competence protein ComEC

Query Match
Best Local Similarity 56.7%; Score 38; DB 2; Length 754;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 AGTATGGG 12
DB 240 AGTATGGG 248

RESULT 35
S76592
5-methyltetrahydrofolate-homocysteine S-methyltransferase (EC 2.1.1.13) [similarity] - *Synechocystis*
C:Species: *Synechocystis* sp.
A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C:Accession: S76592
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis* sp.
A:Reference number: S74322; MUID:97061201; PMID:8905231
A:Accession: S76592
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1195 <KAN>
A:Cross-references: UNIPROT:Q55786; EMBL:D44002; GB:AB001339; NID:gl001612; PIDN:BA11043
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C:Superfamily: cobalamin-dependent methionine synthase; cobalamin-binding homology
C:Keywords: methyltransferase
F:737/Binding site: methylcobalamin cobalt (His) (axial ligand) #status predicted

Query Match
Best Local Similarity 56.7%; Score 38; DB 2; Length 1195;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 EFGAGLVG 9
DB 456 EFGAGLVG 464

RESULT 36
D64012
hypothetical protein H10704 - *Haemophilus influenzae* (strain Rd KW20)
C:Species: *Haemophilus influenzae*
A:Variety: strain Rd KW20
C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
C:Accession: D64012; T09409
R:Feilschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kierlavage, A.

Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M. Science 269, 496-512, 1995
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A.; Title: Whole-genome random sequencing and assembly of *Haemophilus influenzae* Rd.
A:Reference number: A64000; MUID:95350630; PMID:7542800
A:Accession: D64012
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-61 <RIG>
A:Cross-references: UNIPROT:P44040; GB:U32753; GB:L42023; NID:gl573701; PIDN:AAC2367.1; C:Genetics:
A:Note: H10704

Query Match
Best Local Similarity 55.2%; Score 37; DB 2; Length 61;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 GAGLVGGGFM 13
DB 38 GAGLVGGGFM 48

RESULT 37
J50297
infection structure-specific protein - rust fungus (*Uromyces appendiculatus*)
C:Species: *Uromyces appendiculatus*
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
C:Accession: J50297
R:Bhairi, S.M.; Staples, R.C.; Freye, P.; Yoder, O.C.
Gene 81, 237-243, 1989
A:Title: Characterization of an infection structure-specific gene from the rust fungus *Uromyces appendiculatus*
A:Reference number: J50297; MUID:90034196; PMID:2806914
A:Accession: J50297
A:Molecule type: DNA
A:Residues: 1-150 <BHA>
A:Cross-references: UNIPROT:P14777
C:Comment: This protein is involved in the development of infection structures and the cc
C:Genetics:
A:Gene: INF24

Query Match
Best Local Similarity 55.2%; Score 37; DB 2; Length 150;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 FGAGLVGGG 12
DB 24 FGAGLVGGG 34

RESULT 38
AH1737
NADH-dependent FMN reductase homolog lin2445 [imported] - *Listeria innocua* (strain C101)
C:Species: *Listeria innocua*
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C:Accession: AH1737
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baguer, F.; Berche, P.; Bloeker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurgey, O.; Ertan, K.D.; Fehli, H.; Science 294, 849-852, 2001
A:Authors: Kref, J.; Kuhn, M.; Kunst, F.; Kurapat, G.; Madueno, E.; Maitouram, A.; Mat ok, C.; Schueter, T.; Simoes, N.; Tietze, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative genomics of *Listeria* species
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AH1737
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-181 <Gla>
A:Cross-references: UNIPROT:Q92877; GB:AL592022; PIDN:CMC97672.1; PID:gl6414967; GSPDB:GM A:Experimental source: strain C1011262
C:Genetics:
A:Gene: lin2445

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